# THE GENOMES OF BACTERIOPHAGES NY12 AND SAURON

An Undergraduate Research Scholars Thesis

by

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# ABSTRACT

The Genomes of Bacteriophages NY12 and Sauron. (May 2015)

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*Burkholderia cenocepacia* is one of seventeen opportunistic pathogens that form the *Burkholderia cepacia* complex (Bcc). In the clinical environment, Bcc species are especially problematic due to their resistance to many disinfectants and antibiotics. As a result, isolating and characterizing bacteriophages that target these bacteria is becoming increasingly important as an alternative method of treatment. This project focuses on the characterization of NY12 and Sauron, two closely related phages that infect *B. cenocepacia*. Genome comparison software was used to identify phage genes and their likely functions, including predicting lysis genes, mobile elements, and other features. Putative invertible DNA segments in the genomes were identified. These invertible regions were analyzed using PCR and restriction analysis. These inversions may be a novel mechanism for genetic diversity in bacteriophages.

# DEDICATION

To my parents, for all of their support, love, and patience throughout the years.

# ACKNOWLEDGEMENTS

I would like to express my deepest gratitude to Drs. Jason Gill, Ryland Young, and Gabby Everett, and to Jackie Grimm, Adriana Hernandez, Lauren Lessor, Eric Rasche and the entire CPT for all of the help and support that has been given to me over the years.

# CHAPTER I

# INTRODUCTION

*Burkholderia cenocepacia* is one of seventeen opportunistic pathogens that form the Burkholderia cepacia complex (Bcc). Patients with chronic lung diseases or patients who are immunocompromised are at greater risk of infection by these bacteria. In the clinical environment, Bcc species prove especially problematic due to their resistance to many disinfectants and antibiotics (1). They also form biofilms and grow in medical devices, equipment, and water sources, allowing them to spread to and infect vulnerable patients. Isolating and characterizing bacteriophages that target these bacteria is becoming increasingly important as an alternative method of treatment.

Phage therapy has been used since the 1920s to treat bacterial infections including dysentery, cholera, and bubonic plague. However, at that time phage were not well understood and with the development of inexpensive and highly effective antibiotics, phage therapy fell from favor in the United States and most other countries. Interestingly, phage still remain in use in the former Soviet Union. However, due to the increased prevalence of antibiotic resistance, phage therapy is once again being considered as an antibiotic alternative (2). Phage therapy has recently been shown to be a possible treatment option for *B. cenocepacia* infections in a mouse lung model (3).

A significant portion of the foundation for gene structure and regulation has been discovered using bacteriophages. Coliphages such as lambda and the T-series phages have been the focus of decades of work; however, phages outside of this narrow area of well-studied phages are not well

understood. The presence of invertible regions in phage genomes is not unheard of, such as in phage Mu or P1, but they tend to be small and in the center of their genome (4-6). PCR analysis suggested that the two relatively large outer regions in the Sauron genome appear to exist in two orientations. This result was confirmed using another *Burkholderia* phage, NY12. Such inversion has not been previously reported in any bacteriophage. The function of these inversions and their involvement in the life cycle is unknown; however, these inversions may be a novel mechanism for genetic diversity in bacteriophages.

# CHAPTER II

# MATERIALS AND METHODS

## Phage Isolation and Culture

*Burkholderia dolosa* (AU0158) and *B. cenocepacia* strain HI2424 were provided by J. LiPuma from the University of Michigan, School of Public Health.

Phage NY12 was isolated from a soil sample collected from NY, USA in September of 2006 based on its ability to grow on *B. dolosa* (AU0158). NY12 was isolated using a modified direct concentration method (7). Briefly, 400 g of soil were added to 2 L of soil wash buffer (peptone 1 g/L, 20 mM Tris-HCl, pH 7.5) and agitated by hand for 10 min at room temperature. The slurry was allowed to settle for ~30 min. and the supernatant was decanted and centrifuged at 10,000 g, 10ºC for 15 min. This supernatant was clarified by filtration through Whatman #1 paper (Whatman) in a Buchner funnel, and the filtrate was then re-filtered through Whatman #6 paper in the same manner. Eight grams of Whatman DE-52 anion exchange resin were added and incubated at 22°C for 30 min with shaking. The resin was collected in a 50 mL centrifuge tube and centrifuged at 2,000 x g, 2 min, 22°C and the supernatant discarded. The resin was washed twice by resuspension in 45 mL wash buffer (25 mM Tris–HCl, pH 7.5, 10 mM NaCl, 5 mM $MgSO_4$) followed by centrifugation as above. Phage were eluted from the resin by addition of 30 ml elution buffer (25 mM Tris–HCl, pH 7.5, 600 mM NaCl, 5 mM $MgSO_4$) followed by centrifugation as above, and the supernatant was retained and concentrated to a final volume of ~500 µL in a 100 kDa MWCO centrifugal ultrafiltration device (Millipore). This total phage concentrate was then plated on lawns of *B. cenocepacia* HI2424 and observed for plaque

formation. Sauron was isolated in 2000 by enrichment of an extract of 2 g soil obtained from Oswego County, NY using *Burkholderia spp.* strain S198B1A as a host (8). Individual plaques were picked and sub-cultured three times, then propagated to high-titer lysates in soft agar overlays as described above.

**Phage DNA Preparation and Sequencing**

Bacteriophage genomic DNA was prepared from 10 mL of filter-sterilized, high-titer (> 1 x $10^{10}$ PFU/mL) phage lysates using a modified form of the Promega Wizard DNA clean-up kit (Promega) as described previously (9). DNA integrity was verified by electrophoresis on a 0.8% agarose gel and staining with ethidium bromide; DNA was quantified by band densitometry. Phage genome size was estimated by pulse field gel electrophoresis (PFGE) analysis of genomic DNA on a 1% agarose gel (Pulse-field agarose, BioRad) and comparison to a size marker (Lambda Ladder PFG Marker, New England Biolabs). Due to difficulties in sequencing Sauron, whole genomic Sauron DNA was first amplified using the MDA-based GenomiPhi amplification kit (GE Healthcare) following the manufacturer's instructions and using 20 ng of input DNA. Phage genomic DNA was sequenced in indexed libraries by 454 pyrosequencing (Roche) at the Emory GRA Genome Center (Emory University, GA, USA), and by Illumina MiSeq at the Genome Sequencing and Analysis Facility at the University of Texas, Austin. In the case of 454 data, trimmed FLX Titanium flowgram outputs were assembled using the Newbler assembler version 2.0.01.14 or 2.5.3 (454 Life Sciences) at default settings. Illumina data was trimmed using FastX Toolkit and assembled with Velvet version 1.2.10. Phage NY12 was sequenced to an average coverage of 90.6-fold. Phage Sauron was sequenced to an average coverage of 36.9-fold.

**Genome Annotation**

Genes were predicted using GeneMarkS (10) and gene starts were manually edited in Artemis (11). Shine-Delgarno sequences were assessed using the ShineFind tool on the Center for Phage Technology web portal (https://cpt.tamu.edu/cpt-software/portal/gbgenelist.pl). The tRNA genes were predicted by tRNAscan-SE 1.21 (12) and Rho-independent terminators predicted by TransTermHP (13). Proteins were exported and analyzed in batch by BLASTp (14); protein functional characteristics were predicted by batch analysis of all proteins in InterProScan version 4.8 (15). Proteins were additionally analyzed by TMHMM (http://www.cbs.dtu.dk/services/TMHMM), SignalP 4.1 (16), and LipoP 1.0 (17).

**Pulse Field Gels**

Restriction enzyme digests were prepared using 0.5 µg of NY12 DNA and 0.5 µL of restriction enzyme, in addition to the corresponding concentrations of buffer, BSA, and water to a 15 µL total volume reaction. DNA samples were electrophoresed on a 1% gel using Bio-Rad Pulse Field Certified Agarose, 0.5x TBE, and a Bio-Rad CHEF Mapper at 14°C for 7 hours and 53 minutes at a gradient of 6 V/cm, a 120° angle, an initial switch time of 0.06 seconds, a final switch time of 12.02 seconds, and with a linear ramping factor.

The predicted band patterns were made using sequences for the J1AJ2A orientation and J1BJ2B orientation using the ApE A plasmid editor by M. Wayne Davis.

# CHAPTER III

# RESULTS AND DISCUSSION

The myophages BcepNY12 and BcepSauron have 264/263 kb genomes and 445/446 predicted genes respectively, with full details shown in the supplementary information. For NY12, the phage head is approximately 115 nm across, while the tail is 87 nm long while for Sauron the phage head is approximately 117 nm across with an 83 nm long tail (Figure 1). NY12 and Sauron appear to share the greatest similarity both to each other and to the Ralstonia phage RSL1; however many genes also share homology with the bacteriophage T4.

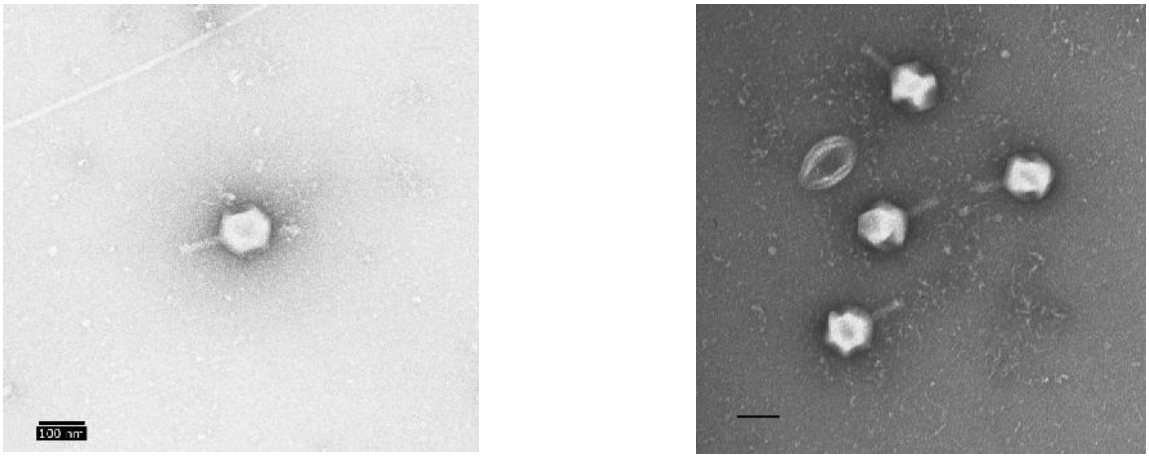


Figure 1: TEM of phages NY12 (left) and Sauron (right). Scale bar: 100 nm.

NY12 produces small, turbid plaques when grown on a lawn of *B. cepacia* strain HI2424. When grown in liquid culture at a multiplicity of infection (MOI) of 0.05, the culture remained turbid throughout the incubation period even while producing a final titer of approximately $5x10^9$ pfu/mL after 14 hours and it remained turbid upon addition of chloroform (Figure 2). Samples

inoculated with NY12 at MOI 0.05 did not appear to have significantly different growth curves than bacteria-only growth samples, nor did they appear to have any significant differences in appearance when examined under the microscope.

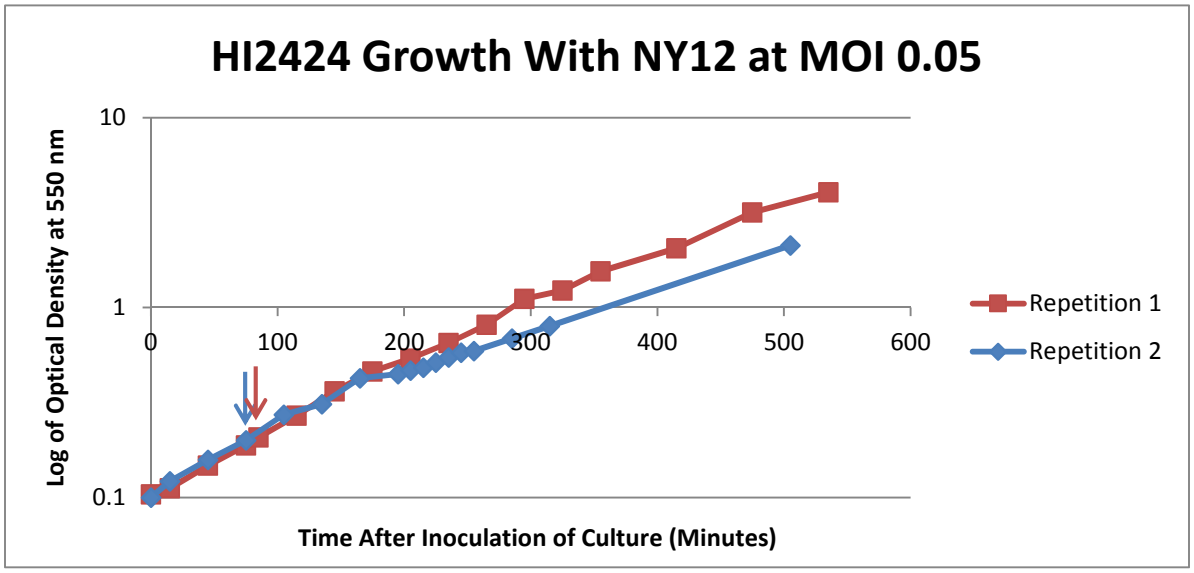


Figure 2: Growth curve of H12424 culture grown at 30°C. Optical density was measured at 550 nm. When the culture reached an O.D. of 0.2, phages were added at MOI 0.05 as denoted by the arrows on the graph.

**Mobile Elements**

Mobile DNA elements are common in bacteriophages. In NY12 there are six predicted homing endonucleases at genes *70, 91, 128, 164, 229, and 236*. In Sauron there are five predicted homing endonucleases at genes *70, 127, 205, 224, and 254*. These endonucleases are spread throughout the genome and represent both HNH and GIY-YIG homing endonucleases. An HNH homing endonuclease contains two pairs of conserved histidines with a conserved asparagine between them (18, 19). A GIY-YIG homing endonuclease contains the sequence GIY followed by ten to eleven amino acids, followed by the sequence YIG (20). These homing endonucleases do not

appear to interrupt any known genes, but interruption of novel hypothetical genes is possible. In addition to homing endonucleases, another type of mobile element found in phage genomes is inteins. Inteins are proteins that are capable of self-excising themselves post-translationally from a host protein. The predicted inteins were discovered using Interpro due to a conserved C-terminal splicing domain (IPR006141) and Hint domain toward the C-terminal end of genes *BcepNY12 170* and *BcepSauron 169*. These genes encode Gyr-B-like type IIA DNA topoisomerases that are likely an example of an essential gene that would increase the likelihood of retention of the intein. It bears sequence similarity to a predicted gene in RSL1, but the closest similarity without the predicted intein is found in *Thermotoga thermarum*. Comparing these sequences suggests that if there is an intein, it may lie between residues 527-698 in NY12 and 531-702 in Sauron. However, this does not match canonical intein boundaries except for n-terminal CN at residue 698 in NY12 and 702 in Sauron; otherwise boundaries are difficult to determine without further experimental evidence.

**Lysis Genes**

Genomic analysis revealed a lysis cassette from genes *BcepNY12 282* to *284* and *BcepSauron 283* to *285*. Genes *BcepNY12 282* and *BcepSauron 283* encode a glycoside hydrolase member of family 19, the chitinases (IPR000726). Chitin and peptidoglycan are structurally very similar. Chitin is a homopolymer of N-acetyl-D-glucosamine linked by β1,4-glycosidic linkages, while peptidoglycan is a heteropolymer of N-acetylglucosamine and N-acetylgalactosamine linked by β1,4-glycosidic linkages. Thus both this and its proximity to the other lysis genes suggest that these genes may function as soluble endolysins (21). Genes *BcepNY12 283* and *BcepSauron 284* appear to encode the antiholin for the predicted holin, the product of *BcepNY12 284* and

*BcepSauron 285*. Holins, upon activation during lysis, form holes in the inner bacterial membrane and allow the endolysin access to the peptidoglycan layer. Antiholins, in contrast, function to inhibit the holin and thus inhibit lysis. The predicted holins, genes *BcepNY12 284* and *BcepSauron 285*, exhibit the N-terminus out, C-terminus in topology of the class I type holin. Unlike in lambda, where the holin and antiholin have a dual start motif, this holin-antiholin pair appear to be two separate, but adjacent, genes. Spanins are proteins that span the entire periplasm and are hypothesized to be involved in the disruption of the outer membrane. In lambda, the two component spanin system contains two embedded genes (22). However in NY12 these genes appear to be two separate genes: the putative i-spanin, gene 226, and o-spanin, gene 227. Unlike the other lysis genes, the spanin genes do not appear to be a part of this predicted lysis cassette. Rather they appear to be clustered within a set of early replication genes including a putative DNA primase gene (*BcepNY12 225/BcepSauron 228*) and DNA polymerase I gene (*BcepNY12 222/BcepSauron 225*). According to one current spanin model, the spanins remain trapped in the peptidoglycan until the holin triggers and allows the endolysin to degrade the cell wall. Thus, this placement of the spanin genes and their potential early expression may not significantly impact the infection cycle (23).

**(p)ppGpp Synthetase**

Guanosine tetraphosphate (ppGpp) functions as an alarmone in *Escherichia coli* during nutrient and amino acid starvation. Under normal conditions, ppGpp is synthesized by the enzyme RelA and is degraded by SpoT. However, during starvation, degradation by SpoT of ppGpp becomes inhibited and ppGpp begins to accumulate. When ppGpp accumulates, rRNA and tRNA synthesis is reduced while other genes involved in stress response are turned on (24).

NY12 and Sauron contain putative ppGpp synthase encoding genes, *BcepNY12 436 and BcepSauron 438*, which suggests that these phages may be affecting the stress response of the host cell. There are many possibilities as to why the phage would benefit from affecting the host stress response. For example, the phage would benefit if it was able to degrade ppGpp and remove the host from the stationary phase, encouraging cell growth for the phage to utilize in its own replication. However, if ppGpp is being synthesized, it is possible that rather than pulling the cell from the stationary phase or removing the host from its stress response, the phage is utilizing some of the pathways involved in the stress response itself. For example, it could be utilizing certain chaperones or transcription factors from the host cell.

**Superinfection Exclusion Proteins**

Two superinfection exclusion proteins were identified at genes *BcepNY12 411* and *412* and *BcepSauron 413* and *414*. Superinfection exclusion refers to the process by which one bacteriophage that has infected a host cell can prevent DNA injection into the cell by other bacteriophages. These genes are notable in that they bear sequence similarity to other immunity to superinfection genes in other bacteriophages and also to the *imm* gene of the phage T4 (protein blast when constrained to T4 gives E=7 x $10^{-5}$ and 1 x $10^{-7}$ respectively for NY12 genes *411* and *412*, and E= 5 x $10^{-7}$and 9 x $10^{-7}$ respectively for Sauron genes *413* and *414*). The *imm* and *sp* genes of T4 are involved in superinfection exclusion. The gene *sp* or "*spackle*" may protect the murein layer from 5-lysozyme (25). In contrast, the gene *imm* is hypothesized to protect the cell via the inner membrane layer (26). No apparent *spackle* homologues were discovered in NY12 or Sauron. As in *imm* gene of T4, genes *BcepNY12 411* and *412* and *BcepSauron 413* and *414* appear to encode transmembrane domains, which may contribute to their mechanism of action.

NY12 may possess a lysis inhibition system as demonstrated the turbidity of the phage cultures even when they contain considerable levels of phage. This is supported by the presence of imm-like proteins which play a role in the T4 lysis inhibition system. However, as the culture does not clear upon addition of chloroform, if there is a lysis inhibition system, it appears to function by a different mechanism than that of T4.

**Potential Invertible DNA Regions**

The 454 sequencing of NY12 returned three contig regions, which were arbitrarily numbered 1, 2, and 3. Forward and reverse primers for the contig ends, designated F and R respectively, were constructed to determine the order and orientation of the contigs. PCR using these primer pairings resulted in products for both F1F3 and F1R3, and F2R1 and R1R2 (Figure 3). The PCR products were sequenced and aligned to determine the order of the contigs. Contigs 2 and 3 were determined to be the outer contigs with contig 1, the largest contig, in the center. Because both orientations of contigs 2 and 3 appear to be able to form a PCR product, the outer contigs may exist in two possible orientations (Figure 4). The middle and largest contig, contig 1, does not appear to be able to invert. Similar results were achieved with Sauron. PCR products for NY12 were also obtained for a pairing between contigs designated 1 and 3 with themselves. These may be non-specific products as a result of weak pairings between regions of the contig, but this requires further investigation.

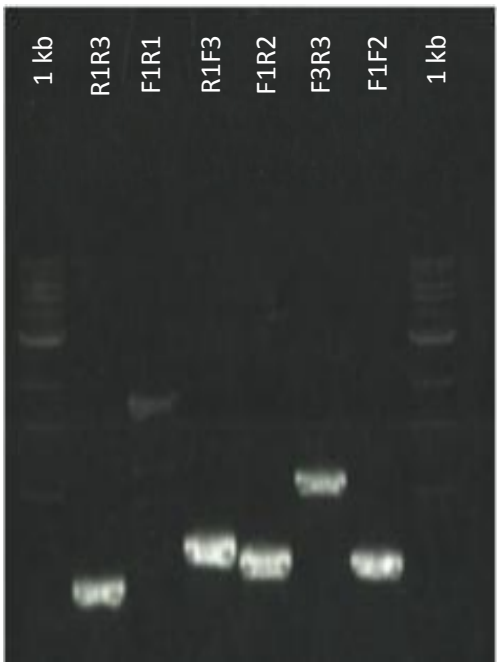


Figure 3: PCR results of contig pairings on a 1% agarose gel.

F indicates a forward primer. R indicates a reverse primer. The primer numbers correlate to numbers randomly assigned to each of the three contigs.

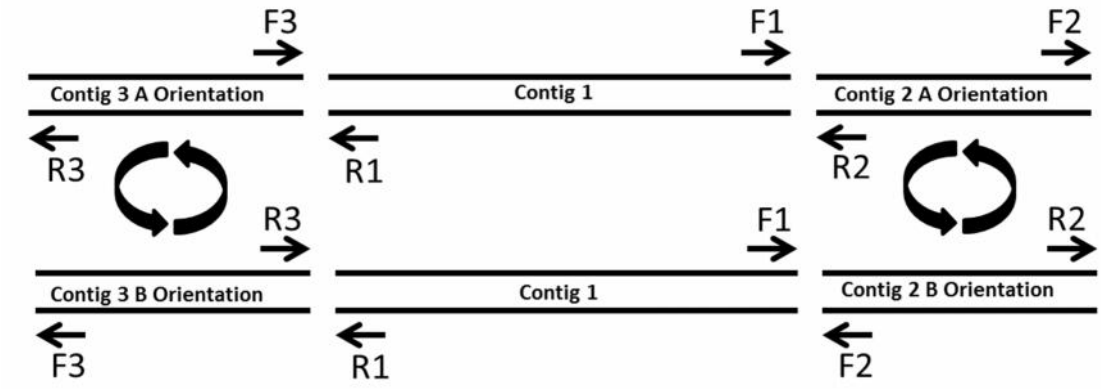


Figure 4: Proposed model of invertible genome segments in NY12 and Sauron.

Restriction analysis was used to further determine if these invertible contigs were present in the actual phage rather than just the PCR product. DNA obtained from phage lysates of NY12 was

digested using restriction enzymes that were expected to produce fragments crossing the supposed “junctions” where the inversions would occur. These fragments would vary in size depending on the orientation of the DNA, and thus the cut sites, in the phage genome. The restriction sites and thus restriction enzymes that would demonstrate this change were limited. While the spacing between bands did vary as expected with a pulse field gel, the pattern itself remained intact and represented the expected band patterns for not only one, but both orientations for these two junctions, designated junctions 1 and 2, with possible orientations A or B (Figures 5 and 6). This leads to the conclusion that both orientations of these regions of DNA are not only possible but present in the bacteriophage NY12.

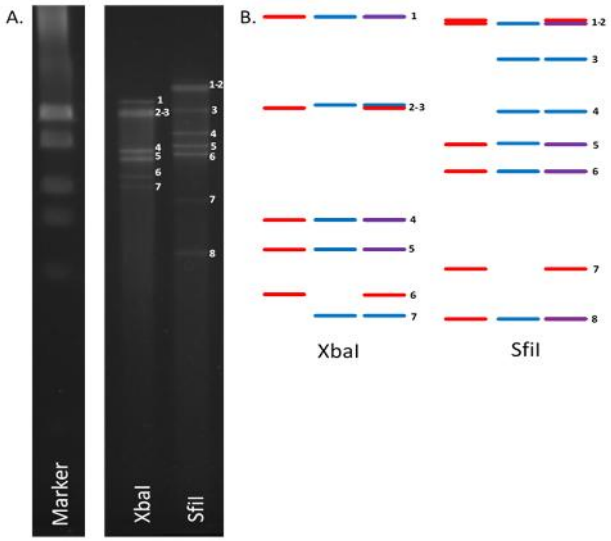


Figure 5. Junction 2

A. Pulse field gel of digested NY12

B. Predicted banding pattern for DNA digests. Red represents orientation J1AJ2A, blue represents J1BJ2B, and purple represents overlapping bands.

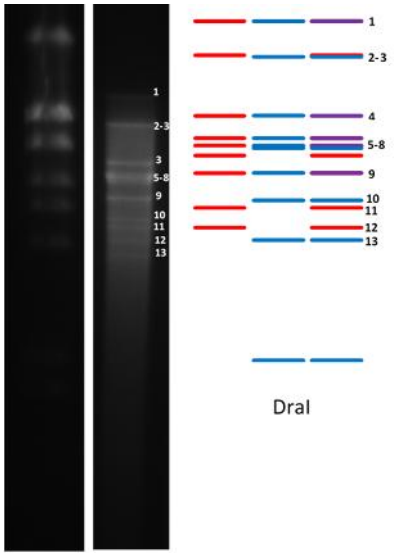


Figure 6. Junction 1

A. Pulse field gel of digested NY12

B. Predicted banding pattern for DNA digests. Red represents orientation J1AJ2A, blue represents J1BJ2B, and purple represents overlapping bands.

The pulse field gels also indicate that the DNA is linear (Figure 7). If the DNA was circular, a different banding pattern would have resulted, as represented in Figure 7.

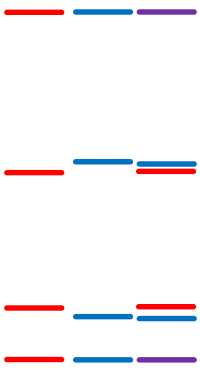

Figure 7: Predicted banding pattern for DNA digest using *Xba*I and a circular NY12 genome

Red represents orientation J1AJ2A, blue represents J1BJ2B, and purple represents overlapping bands.

The purpose of the multiple orientations may lie within the changes that these orientations bring. Both junction boundaries interrupt predicted genes. As shown in figure 8, when contigs two or three change from the A to the B orientation, part of the DNA sequence becomes replaced with another DNA sequence. In addition, some predicted genes are shortened or lengthened by changes in stop codon placement. Some genes, such as *BcepNY12* 445, become parts of other coding sequences rather than being separate genes. Thus, these multiple orientations may add diversity to a single phage strain without changing the nucleic acids themselves. It also may somehow benefit the infectious capabilities of the phage, similar to how the inversion of the G segment in bacteriophage Mu affects the host range specificity in bacteriophage Mu (27). However the functions of the genes affected by the orientation change are currently unknown.

To purify the phage and perform proteomic analysis, a cesium chloride gradient for NY12 was attempted (7). However, the solution became quite viscous and did not form an even band. It is possible that the phage were not able to tolerate the change in osmolarity and that the phage heads burst as a result, leading to the viscous solution. In the future, alternative methods may be required for the phage purification.

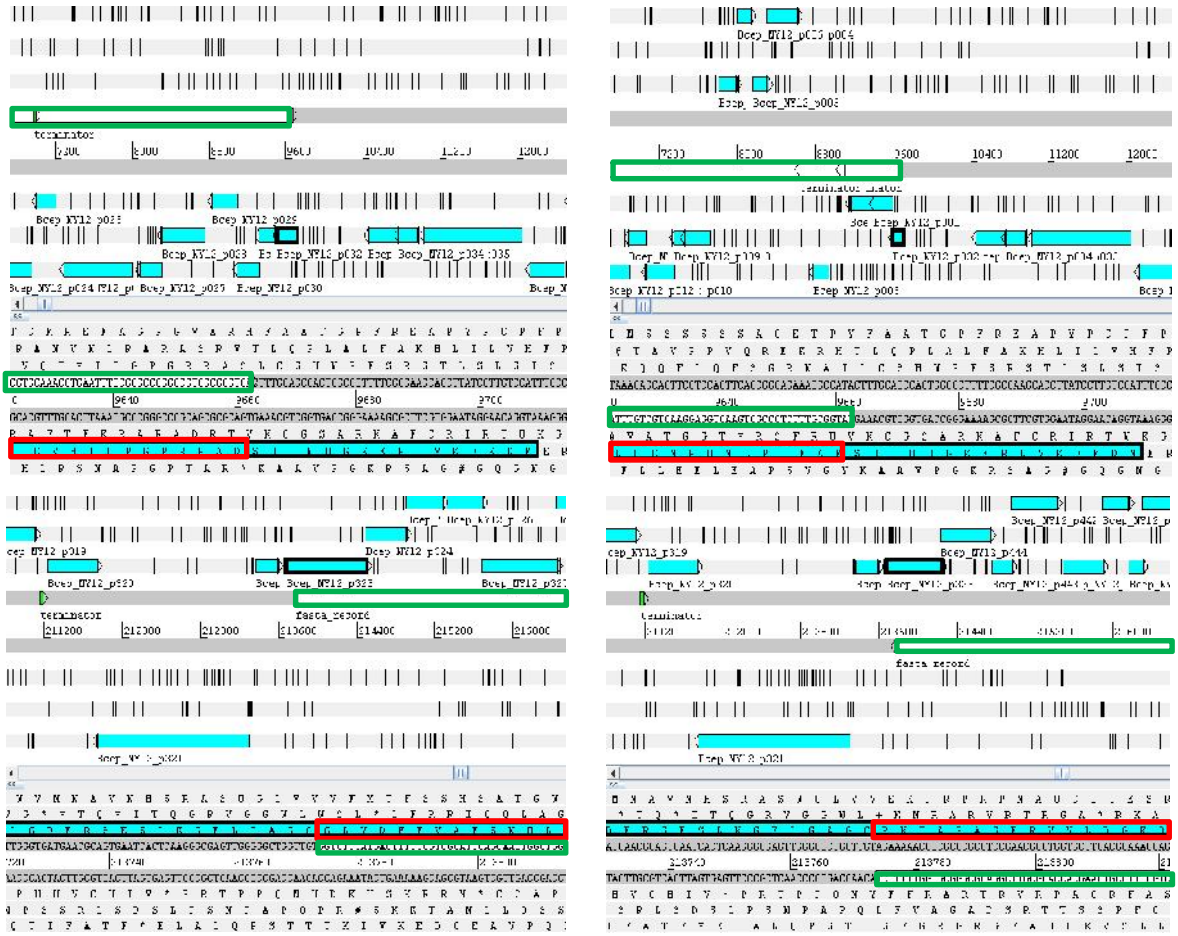

Figure 8: Artemis viewer showing how changing contig orientation alters gene products in NY12
Top left: gene *32* with contig 3 in A orientation. Top right: gene *32* with contig 3 in B orientation. Bottom left: gene *323* with contig 2 in A orientation. Bottom right: gene *323* with contig 2 in B orientation. The green box represents the contig undergoing the orientation change. The red box represents changes to the amino acid sequence of the gene.

# CHAPTER IV

# CONCLUSIONS

Two bacteriophages, NY12 and Sauron, were characterized for the medically-important bacteria *Burkholderia cepacia*. The 445/446 predicted genes were annotated and homology was detected between these phages and both the *Ralstonia* phage RSL1 and T4. One feature of note is the predicted spanin genes being located near early replication genes, separated from the lysis cassette.

A possible novel mechanism was identified for genetic diversity in bacteriophages. Surprisingly, both PCR and restriction analysis support the presence of invertible outer contigs whose junctions cross predicted coding sequences. Further work to investigate these invertible contigs is ongoing.

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# SUPPLEMENTAL

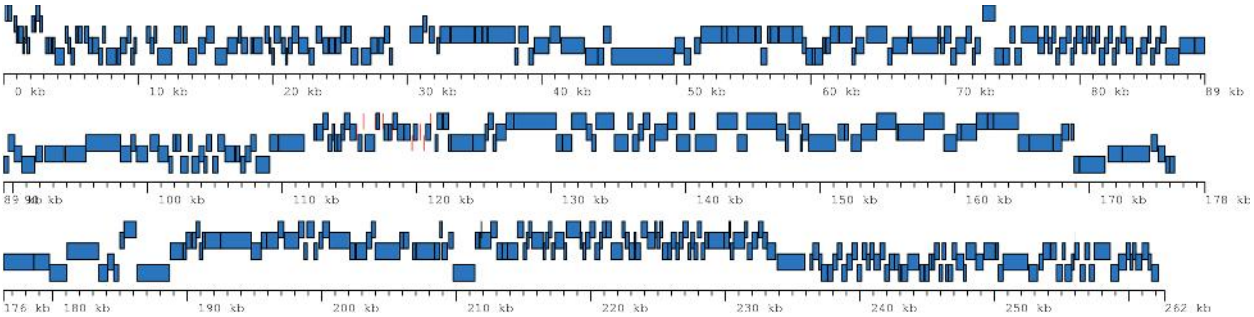

Figure 9: Sauron Genome Map

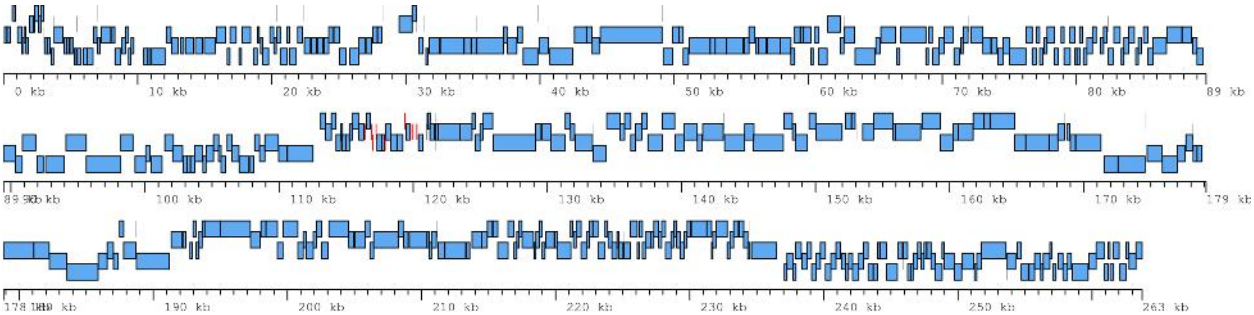

Figure 10: NY12 Genome Map

Table 1: NY12 Annotation Table

| Gene | Match to Sauron | E Value | Putative Function |
|---|---|---|---|
| NY12 p001 | Sauron p001 | 4E-40 | Hypothetical |
| NY12 p002 | Sauron p002 | 1E-51 | Hypothetical |
| NY12 p003 | Sauron p003 | 7E-32 | Hypothetical |
| NY12 p004 | Sauron p005 | 2E-71 | Hypothetical |
| NY12 p005 | Sauron p006 | 3E-24 | Hypothetical |
| NY12 p006 | Sauron p007 | 1E-29 | Hypothetical |
| NY12 p007 | Sauron p008 | 3E-37 | Hypothetical |
| NY12 p008 | Sauron p009 | 2E-43 | Hypothetical |
| NY12 p009 | Sauron p010 | 4E-15 | Hypothetical |
| NY12 p010 | Sauron p011 | 2E-67 | Hypothetical |
| NY12 p011 | Sauron p012 | 8E-39 | Hypothetical |
| NY12 p012 | None | n/a | Hypothetical |

| Gene | Match to Sauron | E Value | Putative Function |
|---|---|---|---|
| NY12 p013 | Sauron p013 | 3E-43 | Hypothetical |
| NY12 p014 | Sauron p014 | 3E-44 | Hypothetical |
| NY12 p015 | Sauron p015 | 1E-33 | Hypothetical |
| NY12 p016 | Sauron p016 | 3E-126 | Hypothetical |
| NY12 p017 | Sauron p017 | 6E-45 | Hypothetical |
| NY12 p018 | Sauron p018 | 9E-37 | Hypothetical |
| NY12 p019 | Sauron p019 | 5E-49 | Hypothetical |
| NY12 p020 | Sauron p020 | 5E-33 | Hypothetical |
| NY12 p021 | Sauron p021 | 2E-64 | Hypothetical |
| NY12 p022 | Sauron p023 | 2E-68 | Hypothetical |
| NY12 p023 | Sauron p024 | 7E-100 | Hypothetical |
| NY12 p024 | Sauron p025 | 8E-56 | Hypothetical |
| NY12 p025 | Sauron p026 | 9E-45 | Hypothetical |
| NY12 p026 | Sauron p027 | 1E-176 | Hypothetical |
| NY12 p027 | Sauron p028 | 8E-50 | Hypothetical |
| NY12 p028 | Sauron p029 | 4E-102 | Hypothetical |
| NY12 p029 | Sauron p030 | 5E-51 | Hypothetical |
| NY12 p030 | Sauron p031 | 2E-48 | Hypothetical |
| NY12 p031 | Sauron p032 | 1E-37 | Hypothetical |
| NY12 p032 | None | n/a | Hypothetical |
| NY12 p033 | Sauron p033 | 4E-55 | Hypothetical |
| NY12 p034 | Sauron p034 | 2E-25 | Hypothetical |
| NY12 p035 | Sauron p035 | 0 | Hypothetical |
| NY12 p036 | None | n/a | Hypothetical |
| NY12 p037 | Sauron p037 | 6E-116 | Hypothetical |
| NY12 p038 | Sauron p038 | 2E-56 | Hypothetical |
| NY12 p039 | Sauron p039 | 7E-127 | Hypothetical |
| NY12 p040 | Sauron p040 | 7E-127 | Hypothetical |
| NY12 p041 | Sauron p042 | 0 | Hypothetical |
| NY12 p042 | Sauron p043 | 4E-154 | Hypothetical |
| NY12 p043 | Sauron p044 | 2E-40 | Hypothetical |
| NY12 p044 | Sauron p045 | 1E-110 | Hypothetical |
| NY12 p045 | Sauron p046 | 2E-22 | Hypothetical |
| NY12 p046 | Sauron p047 | 1E-151 | Hypothetical |
| NY12 p047 | Sauron p048 | 3E-66 | Hypothetical |
| NY12 p048 | Sauron p049 | 1E-27 | Hypothetical |
| NY12 p049 | Sauron p050 | 7E-29 | Hypothetical |
| NY12 p050 | Sauron p051 | 2E-108 | Hypothetical |
| NY12 p051 | Sauron p052 | 6E-68 | Hypothetical |
| NY12 p052 | Sauron p053 | 4E-30 | Hypothetical |
| NY12 p053 | Sauron p054 | 3E-58 | Hypothetical |
| NY12 p054 | Sauron p055 | 8E-119 | Hypothetical |

| Gene | Match to Sauron | E Value | Putative Function |
|---|---|---|---|
| NY12 p055 | Sauron p056 | 8E-44 | Hypothetical |
| NY12 p056 | Sauron p056 | 3E-119 | Hypothetical |
| NY12 p057 | Sauron p057 | 2E-84 | Hypothetical |
| NY12 p058 | Sauron p058 | 1E-96 | Hypothetical |
| NY12 p059 | Sauron p059 | 6E-88 | Hypothetical |
| NY12 p060 | Sauron p060 | 7E-85 | Hypothetical |
| NY12 p061 | Sauron p061 | 3E-83 | Hypothetical |
| NY12 p062 | Sauron p062 | 8E-69 | Hypothetical |
| NY12 p063 | Sauron p063 | 5E-99 | Hypothetical |
| NY12 p064 | Sauron p064 | 2E-123 | Hypothetical |
| NY12 p065 | Sauron p065 | 5E-143 | Hypothetical |
| NY12 p066 | Sauron p066 | 8E-110 | Hypothetical |
| NY12 p067 | Sauron p067 | 5E-87 | Hypothetical |
| NY12 p068 | Sauron p068 | 1E-80 | Hypothetical |
| NY12 p069 | None | n/a | Hypothetical |
| NY12 p070 | Sauron p070 | 0 | Homing Endonuclease (GIY-YIG) |
| NY12 p071 | Sauron p071 | 2E-68 | Hypothetical |
| NY12 p072 | Sauron p072 | 7E-78 | Hypothetical |
| NY12 p073 | Sauron p073 | 4E-35 | Hypothetical |
| NY12 p074 | Sauron p074 | 0 | Hypothetical |
| NY12 p075 | Sauron p075 | 0 | Hypothetical |
| NY12 p076 | Sauron p076 | 6E-124 | Tail Tube Protein |
| NY12 p077 | Sauron p077 | 1E-81 | Hypothetical |
| NY12 p078 | Sauron p078 | 0 | Tail Sheath Protein |
| | Sauron p265 | 0.00000006 | Base Plate Wedge Subunit |
| NY12 p079 | Sauron p079 | 4E-56 | Hypothetical |
| NY12 p080 | Sauron p080 | 8E-175 | Hypothetical |
| NY12 p081 | Sauron p081 | 3E-77 | Hypothetical |
| NY12 p082 | Sauron p082 | 0 | Hypothetical |
| | Sauron p292 | 0.000008 | Hypothetical |
| NY12 p083 | Sauron p083 | 5E-171 | Hypothetical |
| NY12 p084 | Sauron p084 | 0 | Hypothetical |
| NY12 p085 | Sauron p085 | 0 | Hypothetical |
| NY12 p086 | Sauron p086 | 2E-94 | Hypothetical |
| NY12 p087 | Sauron p087 | 2E-66 | Hypothetical |
| NY12 p088 | Sauron p088 | 0 | SNF2-like Helicase |
| NY12 p089 | Sauron p089 | 2E-178 | Hypothetical |
| NY12 p090 | Sauron p090 | 3E-106 | Hypothetical |
| NY12 p091 | Sauron p163 | 0.0005 | HNH Endonuclease |
| NY12 p092 | Sauron p091 | 5E-76 | Hypothetical |
| NY12 p093 | Sauron p092 | 2E-96 | Hypothetical |
| NY12 p094 | Sauron p093 | 0 | Hypothetical |

| Gene | Match to Sauron | E Value | Putative Function |
|---|---|---|---|
| NY12 p095 | Sauron p094 | 1E-87 | Hypothetical |
| NY12 p096 | Sauron p095 | 0 | Hypothetical |
| NY12 p097 | Sauron p096 | 3E-88 | Hypothetical |
| NY12 p098 | Sauron p097 | 2E-110 | Cytidine/Deoxycytidine Deaminase |
| NY12 p099 | Sauron p098 | 4E-48 | Hypothetical |
| NY12 p100 | Sauron p099 | 9E-139 | NUDIX Hydrolase Domain |
| NY12 p101 | Sauron p100 | 0 | Hypothetical |
| NY12 p102 | Sauron p101 | 8E-107 | Hypothetical |
| NY12 p103 | Sauron p102 | 4E-65 | Hypothetical |
| NY12 p104 | Sauron p103 | 1E-36 | Hypothetical |
| NY12 p105 | Sauron p104 | 3E-48 | Hypothetical |
| NY12 p106 | Sauron p105 | 9E-134 | Hypothetical |
| NY12 p107 | Sauron p106 | 2E-33 | Hypothetical |
| NY12 p108 | Sauron p107 | 3E-47 | Hypothetical |
| NY12 p109 | Sauron p108 | 2E-161 | Hypothetical |
| NY12 p110 | Sauron p109 | 0 | Kelch-motif Containing Protein |
| NY12 p111 | Sauron p110 | 1E-56 | Hypothetical |
| NY12 p112 | Sauron p111 | 6E-139 | Hypothetical |
| NY12 p113 | Sauron p112 | 0 | Nicotinate Phosphoribosyltransferase |
| NY12 p114 | Sauron p113 | 3E-74 | Hypothetical |
| NY12 p115 | Sauron p114 | 0 | Putative Cytidyltransferase |
| | Sauron p131 | 0.00004 | NUDIX Hydrolase |
| NY12 p116 | Sauron p115 | 2E-49 | Hypothetical |
| NY12 p117 | Sauron p116 | 0 | NAD-dependent DNA Ligase |
| NY12 p118 | Sauron p117 | 1E-40 | Hypothetical |
| NY12 p119 | Sauron p118 | 3E-56 | Acyl Carrier Protein-like |
| NY12 p120 | Sauron p119 | 7E-109 | Hypothetical |
| NY12 p121 | Sauron p120 | 1E-98 | Hypothetical |
| NY12 p122 | Sauron p121 | 4E-167 | Hypothetical |
| NY12 p123 | Sauron p122 | 2E-96 | Hypothetical |
| NY12 p124 | Sauron p123 | 6E-38 | Hypothetical |
| NY12 p125 | Sauron p124 | 4E-84 | Hypothetical |
| NY12 p126 | Sauron p125 | 0 | Hypothetical |
| NY12 p127 | Sauron p126 | 2E-148 | Putative Phosphatase |
| NY12 p128 | Sauron p127 | 7E-106 | HNH Endonuclease |
| NY12 p129 | Sauron p128 | 1E-84 | Hypothetical |
| NY12 p130 | Sauron p129 | 4E-111 | Aspartyl/glutamyl-tRNA Amidotransferase Subunit B-like |
| NY12 p131 | Sauron p130 | 0 | RtcB-like Protein |
| NY12 p132 | Sauron p131 | 8E-102 | NUDIX Hydrolase |
| NY12 p133 | Sauron p132 | 3E-71 | Hypothetical |
| NY12 p134 | Sauron p133 | 7E-59 | Hypothetical |
| NY12 p135 | Sauron p134 | 9E-59 | Hypothetical |

| Gene | Match to Sauron | E Value | Putative Function |
|---|---|---|---|
| NY12 p136 | Sauron p135 | 5E-48 | Hypothetical |
| NY12 p137 | Sauron p136 | 4E-126 | Hypothetical |
| NY12 p138 | Sauron p137 | 3E-71 | Hypothetical |
| NY12 p139 | Sauron p139 | 1E-50 | Hypothetical |
| NY12 p140 | Sauron p140 | 1E-110 | Hypothetical |
| NY12 p141 | Sauron p141 | 5E-84 | Hypothetical |
| NY12 p142 | Sauron p142 | 3E-35 | Hypothetical |
| NY12 p143 | Sauron p143 | 6E-48 | Hypothetical |
| NY12 p144 | Sauron p144 | 1E-51 | Hypothetical |
| NY12 p145 | Sauron p145 | 2E-62 | Hypothetical |
| NY12 p146 | Sauron p146 | 3E-99 | Hypothetical |
| NY12 p147 | Sauron p147 | 1E-65 | Hypothetical |
| NY12 p148 | Sauron p149 | 2E-54 | Hypothetical |
| | Sauron p150 | 1E-12 | Hypothetical |
| NY12 p149 | Sauron p150 | 7E-49 | Hypothetical |
| | Sauron p149 | 2E-10 | Hypothetical |
| NY12 p150 | Sauron p151 | 1E-77 | Hypothetical |
| | Sauron p037 | 0.0007 | Hypothetical |
| NY12 p151 | Sauron p152 | 7E-109 | Hypothetical |
| NY12 p152 | None | n/a | Hypothetical |
| NY12 p153 | Sauron p153 | 7E-67 | Hypothetical |
| NY12 p154 | Sauron p154 | 4E-105 | Hypothetical |
| NY12 p155 | Sauron p155 | 7E-45 | Hypothetical |
| NY12 p156 | Sauron p156 | 4E-52 | Hypothetical |
| NY12 p157 | Sauron p157 | 7E-56 | Hypothetical |
| NY12 p158 | Sauron p158 | 3E-89 | Hypothetical |
| NY12 p159 | Sauron p159 | 0 | Hypothetical |
| NY12 p160 | Sauron p160 | 0 | Putative RNA Ligase |
| NY12 p161 | Sauron p161 | 9E-178 | Hypothetical |
| NY12 p162 | Sauron p162 | 6E-80 | Hypothetical |
| NY12 p163 | Sauron p163 | 9E-112 | Hypothetical |
| NY12 p164 | Sauron p254 | 3E-22 | Putative Homing Endonuclease |
| NY12 p165 | Sauron p164 | 2E-125 | Hypothetical |
| NY12 p166 | Sauron p165 | 0 | Hypothetical |
| NY12 p167 | Sauron p166 | 4E-20 | Hypothetical |
| NY12 p168 | Sauron p167 | 0 | Hypothetical |
| NY12 p169 | Sauron p168 | 0 | Type IIA DNA Topoisomerase, GyrA-like |
| | Sauron p180 | 0.0005 | Hypothetical |
| NY12 p170 | Sauron p169 | 0 | Type IIA DNA Topoisomerase, GyrB-like |
| NY12 p171 | None | n/a | Hypothetical |
| NY12 p172 | Sauron p170 | 0 | Hypothetical |
| NY12 p173 | Sauron p171 | 4E-73 | Hypothetical |

| Gene | Match to Sauron | E Value | Putative Function |
|---|---|---|---|
| NY12 p174 | Sauron p172 | 4E-78 | Hypothetical |
| NY12 p175 | Sauron p173 | 4E-155 | Hypothetical |
| NY12 p176 | Sauron p174 | 0 | Hypothetical |
| NY12 p177 | Sauron p175 | 8E-62 | Hypothetical |
| NY12 p178 | Sauron p176 | 4E-44 | Hypothetical |
| NY12 p179 | Sauron p177 | 6E-72 | Hypothetical |
| NY12 p180 | Sauron p178 | 5E-122 | Hypothetical |
| NY12 p181 | Sauron p179 | 5E-43 | Hypothetical |
| NY12 p182 | Sauron p180 | 1E-129 | Hypothetical |
| | Sauron p168 | 0.0005 | Type IIA DNA Topoisomerase, GyrA-like |
| NY12 p183 | Sauron p181 | 3E-90 | Hypothetical |
| NY12 p184 | Sauron p182 | 3E-31 | Hypothetical |
| NY12 p185 | Sauron p183 | 4E-81 | Hypothetical |
| NY12 p186 | Sauron p184 | 3E-67 | Hypothetical |
| NY12 p187 | Sauron p185 | 1E-124 | Hypothetical |
| NY12 p188 | Sauron p186 | 9E-178 | Hypothetical |
| | Sauron p192 | 0.0004 | Hypothetical |
| NY12 p189 | Sauron p187 | 1E-63 | Hypothetical |
| NY12 p190 | Sauron p188 | 8E-80 | Hypothetical |
| NY12 p191 | Sauron p190 | 3E-85 | Hypothetical |
| NY12 p192 | Sauron p191 | 0 | Recombination Endonuclease-like Protein |
| NY12 p193 | Sauron p192 | 3E-132 | Hypothetical |
| | Sauron p186 | 0.0005 | Hypothetical |
| NY12 p194 | Sauron p193 | 0 | DEAD Type Helicase |
| | Sauron p384 | 2E-121 | Hypothetical |
| NY12 p195 | None | n/a | Hypothetical |
| NY12 p196 | Sauron p195 | 2E-62 | Hypothetical |
| NY12 p197 | Sauron p196 | 2E-82 | Hypothetical |
| NY12 p198 | Sauron p197 | 2E-71 | Hypothetical |
| NY12 p199 | Sauron p198 | 5E-25 | Hypothetical |
| NY12 p200 | Sauron p199 | 7E-52 | Hypothetical |
| NY12 p201 | Sauron p200 | 2E-62 | Hypothetical |
| NY12 p202 | Sauron p201 | 5E-47 | Hypothetical |
| NY12 p203 | Sauron p202 | 1E-104 | Hypothetical |
| NY12 p204 | Sauron p203 | 5E-97 | Hypothetical |
| NY12 p205 | Sauron p204 | 2E-58 | Hypothetical |
| NY12 p206 | Sauron p207 | 5E-81 | Hypothetical |
| NY12 p207 | Sauron p208 | 5E-45 | Hypothetical |
| NY12 p208 | Sauron p209 | 2E-79 | Hypothetical |
| NY12 p209 | Sauron p210 | 4E-103 | Hypothetical |
| | Sauron p251 | 1E-13 | Hypothetical |
| NY12 p210 | Sauron p211 | 5E-76 | Hypothetical |

| Gene | Match to Sauron | E Value | Putative Function |
|---|---|---|---|
| NY12 p211 | Sauron p212 | 1E-50 | GroES-like Protein |
| NY12 p212 | Sauron p213 | 1E-73 | Thioredoxin |
| NY12 p213 | Sauron p214 | 2E-40 | Hypothetical |
| NY12 p214 | Sauron p215 | 7E-79 | Hypothetical |
| NY12 p215 | Sauron p217 | 9E-39 | Hypothetical |
| NY12 p216 | Sauron p218 | 0 | RecD-like Protein |
| NY12 p217 | Sauron p219 | 0 | Endodeoxyribonuclease |
| NY12 p218 | Sauron p220 | 1E-52 | Hypothetical |
| NY12 p219 | Sauron p221 | 2E-83 | Hypothetical |
| NY12 p220 | Sauron p222 | 8E-55 | Hypothetical |
| NY12 p221 | Sauron p223 | 5E-175 | Metal Dependent Phosphohydrolase-like Protein |
| NY12 p222 | Sauron p225 | 0 | DNA Polymerase I |
| NY12 p223 | Sauron p226 | 7E-101 | Hypothetical |
| NY12 p224 | Sauron p227 | 1E-165 | Hypothetical |
| NY12 p225 | Sauron p228 | 0 | DNA Primase |
| NY12 p226 | Sauron p229 | 5E-94 | Putative i-spanin |
| NY12 p227 | Sauron p230 | 4E-72 | Putative o-spanin |
| NY12 p228 | Sauron p231 | 0 | Hypothetical |
| | Sauron p251 | 0.000004 | Hypothetical |
| NY12 p229 | Sauron p254 | 2E-13 | Homing Endonuclease |
| NY12 p230 | Sauron p232 | 0 | Hypothetical |
| NY12 p231 | Sauron p233 | 2E-82 | Hypothetical |
| NY12 p232 | Sauron p234 | 1E-112 | Hypothetical |
| NY12 p233 | Sauron p235 | 4E-85 | Hypothetical |
| NY12 p234 | Sauron p236 | 6E-111 | Hypothetical |
| NY12 p235 | Sauron p237 | 2E-94 | Hypothetical |
| NY12 p236 | None | n/a | GIY-YIG Endonuclease |
| NY12 p237 | Sauron p238 | 1E-154 | Thymidylate Synthase |
| NY12 p238 | Sauron p239 | 2E-165 | Hypothetical |
| NY12 p239 | Sauron p240 | 0 | Hypothetical |
| NY12 p240 | Sauron p241 | 2E-79 | Hypothetical |
| NY12 p241 | Sauron p242 | 0 | Hypothetical |
| NY12 p242 | Sauron p243 | 0 | RecA-like Recombinase |
| NY12 p243 | Sauron p244 | 3E-171 | Hypothetical |
| NY12 p244 | Sauron p245 | 0 | Terminase |
| NY12 p245 | Sauron p246 | 1E-157 | RuvC Resolvase-like Protein |
| NY12 p246 | Sauron p247 | 1E-53 | Hypothetical |
| NY12 p247 | Sauron p248 | 0 | Hypothetical |
| NY12 p248 | Sauron p250 | 2E-114 | Hypothetical |
| NY12 p249 | Sauron p251 | 0 | Hypothetical |
| | Sauron p210 | 1E-13 | Hypothetical |
| | Sauron p231 | 0.0007 | Hypothetical |

| Gene | Match to Sauron | E Value | Putative Function |
|---|---|---|---|
| NY12 p250 | Sauron p252 | 8E-108 | Hypothetical |
| NY12 p251 | Sauron p253 | 1E-62 | Hypothetical |
| | Sauron p276 | 0.00004 | Hypothetical |
| NY12 p252 | Sauron p255 | 0 | Hypothetical |
| NY12 p253 | Sauron p256 | 0 | Hypothetical |
| NY12 p254 | Sauron p257 | 1E-33 | Hypothetical |
| NY12 p255 | Sauron p258 | 0 | Hypothetical |
| NY12 p256 | Sauron p259 | 0 | Tail Protein |
| NY12 p257 | Sauron p260 | 0 | Hypothetical |
| NY12 p258 | Sauron p261 | 9E-85 | Hypothetical |
| NY12 p259 | Sauron p262 | 0 | Hypothetical |
| NY12 p260 | Sauron p263 | 0 | Hypothetical |
| NY12 p261 | Sauron p264 | 7E-104 | Baseplate Wedge Subunit |
| NY12 p262 | Sauron p265 | 0 | Structural Protein |
| | Sauron p078 | 0.00000006 | Tail Sheath Protein |
| NY12 p263 | Sauron p266 | 0 | Hypothetical |
| NY12 p264 | Sauron p267 | 0 | Phage Tail Protein |
| | Sauron p288 | 5E-15 | Phage Tail Protein |
| NY12 p265 | Sauron p268 | 1E-130 | Hypothetical |
| NY12 p266 | Sauron p269 | 4E-128 | Hypothetical |
| NY12 p267 | Sauron p270 | 7E-51 | Hypothetical |
| NY12 p268 | Sauron p271 | 5E-91 | Hypothetical |
| NY12 p269 | Sauron p272 | 0 | Hypothetical |
| NY12 p270 | Sauron p273 | 0 | Hypothetical |
| | Sauron p280 | 0.0000007 | Hypothetical |
| NY12 p271 | Sauron p274 | 0 | Hypothetical |
| | Sauron p282 | 2E-18 | Hypothetical |
| | Sauron p282 | 0.0003 | Hypothetical |
| | Sauron p288 | 1E-12 | Phage Tail Protein |
| | Sauron p281 | 0.00000003 | Putative Long Tail Fiber Protein |
| | Sauron p281 | 0.000004 | Putative Long Tail Fiber Protein |
| NY12 p272 | Sauron p275 | 2E-106 | Putative Tail Fiber Protein |
| | Sauron p281 | 0.000002 | Putative Long Tail Fiber Protein |
| NY12 p273 | Sauron p281 | 4E-10 | Hypothetical |
| NY12 p274 | Sauron p282 | 0.000000001 | Hypothetical |
| NY12 p275 | Sauron p276 | 1E-117 | Hypothetical |
| | Sauron p253 | 0.00007 | Hypothetical |
| NY12 p276 | Sauron p277 | 4E-66 | Hypothetical |
| NY12 p277 | Sauron p278 | 5E-84 | Hypothetical |
| NY12 p278 | Sauron p279 | 0 | Hypothetical |
| NY12 p279 | Sauron p280 | 0 | Hypothetical |
| | Sauron p273 | 0.000002 | Hypothetical |

| Gene | Match to Sauron | E Value | Putative Function |
|---|---|---|---|
| NY12 p280 | Sauron p281 | 0 | Putative Long Tail Fiber Protein |
| | Sauron p288 | 6E-14 | Phage Tail Protein |
| | Sauron p288 | 4E-11 | Phage Tail Protein |
| | Sauron p288 | 0.000002 | Phage Tail Protein |
| | Sauron p274 | 0.0000002 | Hypothetical |
| | Sauron p274 | 0.000006 | Hypothetical |
| NY12 p281 | Sauron p282 | 0 | Hypothetical |
| | Sauron p274 | 2E-17 | Hypothetical |
| | Sauron p274 | 0.0001 | Hypothetical |
| NY12 p282 | Sauron p283 | 2E-162 | Putative Endolysin (GH19) |
| NY12 p283 | Sauron p284 | 1E-113 | Putative Antiholin |
| NY12 p284 | Sauron p285 | 1E-84 | Putative Type 1 Holin |
| NY12 p285 | Sauron p286 | 1E-68 | Hypothetical |
| NY12 p286 | Sauron p287 | 0 | 5'-3' Exonuclease |
| NY12 p287 | Sauron p288 | 0 | Putative Tail Protein |
| | Sauron p281 | 3E-14 | Putative Long Tail Fiber Protein |
| | Sauron p281 | 9E-11 | Putative Long Tail Fiber Protein |
| | Sauron p281 | 0.000007 | Putative Long Tail Fiber Protein |
| | Sauron p267 | 7E-14 | Phage Tail Collar Protein |
| | Sauron p274 | 2E-12 | Hypothetical |
| NY12 p288 | Sauron p289 | 0 | Hypothetical |
| NY12 p289 | Sauron p290 | 3E-48 | Hypothetical |
| NY12 p290 | None | n/a | Hypothetical |
| NY12 p291 | Sauron p292 | 6E-22 | Hypothetical |
| NY12 p292 | Sauron p293 | 4E-41 | Hypothetical |
| NY12 p293 | Sauron p294 | 3E-54 | Hypothetical |
| NY12 p294 | Sauron p295 | 7E-42 | Hypothetical |
| NY12 p295 | Sauron p296 | 0 | DNA Polymerase III-like Protein |
| NY12 p296 | Sauron p297 | 0 | ATPase Domain Containing Protein |
| NY12 p297 | Sauron p298 | 5E-178 | Hypothetical |
| NY12 p298 | Sauron p299 | 6E-85 | Hypothetical |
| NY12 p299 | Sauron p300 | 0 | Hypothetical |
| NY12 p300 | Sauron p301 | 4E-95 | Hypothetical |
| NY12 p301 | Sauron p302 | 0 | DNA Polymerase III Beta Subunit-like |
| NY12 p302 | Sauron p303 | 3E-98 | Hypothetical |
| NY12 p303 | Sauron p304 | 5E-40 | Hypothetical |
| NY12 p304 | Sauron p305 | 5E-130 | Hypothetical |
| NY12 p305 | Sauron p306 | 4E-48 | Hypothetical |
| NY12 p306 | Sauron p307 | 1E-48 | Hypothetical |
| NY12 p307 | Sauron p308 | 9E-89 | Hypothetical |
| NY12 p308 | Sauron p309 | 0 | ATP-Dependent Helicase |
| NY12 p309 | Sauron p310 | 5E-87 | Hypothetical |

| Gene | Match to Sauron | E Value | Putative Function |
|---|---|---|---|
| NY12 p310 | Sauron p311 | 0 | Hypothetical |
| NY12 p311 | Sauron p312 | 1E-81 | Hypothetical |
| NY12 p312 | Sauron p313 | 1E-63 | Hypothetical |
| NY12 p313 | Sauron p314 | 0 | Hypothetical |
| NY12 p314 | Sauron p316 | 2E-90 | Hypothetical |
| NY12 p315 | Sauron p317 | 3E-47 | Hypothetical |
| NY12 p316 | Sauron p318 | 0 | Replicative DNA Helicase |
| NY12 p317 | None | n/a | Hypothetical |
| NY12 p318 | Sauron p320 | 2E-24 | Hypothetical |
| NY12 p319 | Sauron p321 | 4E-87 | Hypothetical |
| NY12 p320 | Sauron p322 | 3E-10 | Hypothetical |
| NY12 p321 | Sauron p323 | 0 | Hypothetical |
| NY12 p322 | Sauron p324 | 1E-48 | Hypothetical |
| NY12 p323 | None | n/a | Hypothetical |
| NY12 p324 | Sauron p326 | 5E-69 | Hypothetical |
| NY12 p325 | Sauron p327 | 1E-55 | Hypothetical |
| NY12 p326 | Sauron p328 | 4E-45 | Hypothetical |
| NY12 p327 | Sauron p329 | 5E-157 | Hypothetical |
| NY12 p328 | Sauron p330 | 7E-102 | Hypothetical |
| NY12 p329 | Sauron p331 | 3E-46 | Hypothetical |
| NY12 p330 | Sauron p332 | 2E-23 | Hypothetical |
| NY12 p331 | Sauron p333 | 2E-42 | Hypothetical |
| NY12 p332 | Sauron p334 | 8E-145 | tRNA His Guanylyltransferase Thg1 |
| NY12 p333 | Sauron p335 | 1E-30 | Hypothetical |
| NY12 p334 | Sauron p336 | 3E-57 | Hypothetical |
| NY12 p335 | Sauron p337 | 3E-47 | Hypothetical |
| NY12 p336 | Sauron p338 | 6E-46 | Hypothetical |
| NY12 p337 | Sauron p339 | 2E-151 | Hypothetical |
| NY12 p338 | Sauron p340 | 1E-36 | Hypothetical |
| NY12 p339 | Sauron p341 | 0 | Hypothetical |
| | Sauron p325 | 3E-15 | Hypothetical |
| | Sauron p325 | 9E-13 | Hypothetical |
| | Sauron p325 | 0.0003 | Hypothetical |
| NY12 p340 | Sauron p342 | 2E-33 | Hypothetical |
| NY12 p341 | Sauron p343 | 2E-44 | Hypothetical |
| NY12 p342 | Sauron p345 | 3E-69 | Hypothetical |
| | Sauron p400 | 0.00003 | Hypothetical |
| NY12 p343 | Sauron p346 | 7E-34 | Hypothetical |
| | Sauron p344 | 0.00000003 | Hypothetical |
| | Sauron p443 | 0.0005 | Hypothetical |
| NY12 p344 | Sauron p347 | 2E-48 | Hypothetical |
| NY12 p345 | Sauron p348 | 5E-54 | Hypothetical |

| Gene | Match to Sauron | E Value | Putative Function |
|---|---|---|---|
| NY12 p346 | Sauron p349 | 1E-86 | Hypothetical |
| NY12 p347 | Sauron p350 | 5E-113 | Hypothetical |
| NY12 p348 | Sauron p351 | 2E-43 | Hypothetical |
| NY12 p349 | Sauron p352 | 1E-66 | Hypothetical |
| NY12 p350 | Sauron p353 | 5E-68 | Hypothetical |
| NY12 p351 | Sauron p354 | 2E-28 | Hypothetical |
| NY12 p352 | Sauron p355 | 7E-73 | Hypothetical |
| NY12 p353 | Sauron p356 | 3E-108 | Hypothetical |
| NY12 p354 | Sauron p357 | 3E-114 | Hypothetical |
| NY12 p355 | Sauron p358 | 2E-34 | Hypothetical |
| NY12 p356 | Sauron p359 | 1E-50 | Hypothetical |
| NY12 p357 | Sauron p360 | 1E-51 | Hypothetical |
| NY12 p358 | Sauron p361 | 3E-99 | Hypothetical |
| NY12 p359 | Sauron p362 | 1E-49 | Hypothetical |
| NY12 p360 | Sauron p363 | 2E-89 | Hypothetical |
| NY12 p361 | Sauron p364 | 2E-53 | Hypothetical |
| NY12 p362 | Sauron p365 | 1E-68 | Hypothetical |
| NY12 p363 | Sauron p366 | 6E-98 | Hypothetical |
| NY12 p364 | Sauron p367 | 3E-46 | Hypothetical |
| NY12 p365 | Sauron p368 | 2E-54 | Hypothetical |
| NY12 p366 | Sauron p369 | 4E-66 | Hypothetical |
| NY12 p367 | Sauron p370 | 1E-66 | Hypothetical |
| NY12 p368 | Sauron p371 | 8E-53 | Hypothetical |
| NY12 p369 | Sauron p372 | 9E-62 | Hypothetical |
| NY12 p370 | Sauron p373 | 0 | T4 RnlA-like RNA ligase and Tail Fiber Attachment Catalyst |
| NY12 p371 | Sauron p374 | 2E-80 | Hypothetical |
| NY12 p372 | Sauron p375 | 2E-14 | Hypothetical |
| NY12 p373 | Sauron p376 | 2E-54 | Hypothetical |
| NY12 p374 | Sauron p377 | 0 | Putative Nucleotidyltransferase |
| NY12 p375 | Sauron p378 | 3E-14 | Hypothetical |
| NY12 p376 | Sauron p379 | 2E-40 | Hypothetical |
| NY12 p377 | Sauron p380 | 1E-43 | Hypothetical |
| NY12 p378 | Sauron p381 | 8E-79 | Hypothetical |
| NY12 p379 | Sauron p382 | 5E-67 | Hypothetical |
| NY12 p380 | Sauron p383 | 1E-25 | Hypothetical |
| NY12 p381 | Sauron p384 | 0 | Hypothetical |
| | Sauron p193 | 3E-126 | DEAD Type Helicase |
| NY12 p382 | Sauron p385 | 1E-46 | Hypothetical |
| NY12 p383 | Sauron p386 | 2E-101 | Hypothetical |
| NY12 p384 | Sauron p387 | 3E-50 | Hypothetical |
| NY12 p385 | Sauron p388 | 3E-105 | Hypothetical |
| NY12 p386 | Sauron p389 | 0.00000002 | Hypothetical |

| Gene | Match to Sauron | E Value | Putative Function |
|---|---|---|---|
| NY12 p387 | Sauron p389 | 3E-83 | Hypothetical |
| NY12 p388 | Sauron p390 | 5E-81 | Hypothetical |
| | Sauron p392 | 0.000003 | Hypothetical |
| | Sauron p403 | 0.000004 | Hypothetical |
| | Sauron p393 | 0.00004 | Hypothetical |
| | Sauron p391 | 0.0002 | Hypothetical |
| | Sauron p401 | 0.0003 | Hypothetical |
| NY12 p389 | Sauron p391 | 2E-74 | Hypothetical |
| | Sauron p392 | 0.00000001 | Hypothetical |
| | Sauron p401 | 0.00000008 | Hypothetical |
| | Sauron p393 | 0.0000002 | Hypothetical |
| | Sauron p394 | 0.0000009 | Hypothetical |
| | Sauron p402 | 0.00005 | Hypothetical |
| | Sauron p403 | 0.00005 | Hypothetical |
| | Sauron p390 | 0.0002 | Hypothetical |
| | Sauron p395 | 0.0007 | Hypothetical |
| NY12 p390 | Sauron p392 | 6E-90 | Hypothetical |
| | Sauron p393 | 1E-17 | Hypothetical |
| | Sauron p394 | 1E-12 | Hypothetical |
| | Sauron p391 | 0.00000002 | Hypothetical |
| | Sauron p390 | 0.000002 | Hypothetical |
| | Sauron p403 | 0.000007 | Hypothetical |
| NY12 p391 | Sauron p393 | 7E-97 | Hypothetical |
| | Sauron p392 | 3E-20 | Hypothetical |
| | Sauron p394 | 2E-16 | Hypothetical |
| | Sauron p403 | 0.00000002 | Hypothetical |
| | Sauron p391 | 0.0000002 | Hypothetical |
| | Sauron p402 | 0.000002 | Hypothetical |
| | Sauron p390 | 0.00004 | Hypothetical |
| | Sauron p398 | 0.0006 | Hypothetical |
| | Sauron p396 | 0.0009 | Hypothetical |
| NY12 p392 | Sauron p394 | 2E-63 | Hypothetical |
| | Sauron p393 | 2E-15 | Hypothetical |
| | Sauron p392 | 9E-14 | Hypothetical |
| | Sauron p403 | 0.000000006 | Hypothetical |
| | Sauron p401 | 0.000006 | Hypothetical |
| | Sauron p391 | 0.00006 | Hypothetical |
| | Sauron p398 | 0.00007 | Hypothetical |
| NY12 p393 | Sauron p395 | 1E-79 | Hypothetical |
| | Sauron p403 | 0.000002 | Hypothetical |
| NY12 p394 | Sauron p396 | 2E-74 | Hypothetical |
| | Sauron p398 | 2E-10 | Hypothetical |

| Gene | Match to Sauron | E Value | Putative Function |
|---|---|---|---|
| | Sauron p403 | 0.00006 | Hypothetical |
| | Sauron p402 | 0.0001 | Hypothetical |
| | Sauron p394 | 0.0002 | Hypothetical |
| | Sauron p393 | 0.0008 | Hypothetical |
| NY12 p395 | Sauron p397 | 2E-52 | Hypothetical |
| NY12 p396 | Sauron p398 | 3E-72 | Hypothetical |
| | Sauron p396 | 8E-10 | Hypothetical |
| | Sauron p403 | 0.00004 | Hypothetical |
| | Sauron p394 | 0.00007 | Hypothetical |
| | Sauron p401 | 0.0002 | Hypothetical |
| | Sauron p393 | 0.0005 | Hypothetical |
| NY12 p397 | Sauron p399 | 1E-102 | Hypothetical |
| NY12 p398 | Sauron p400 | 7E-59 | Hypothetical |
| | Sauron p402 | 0.00001 | Hypothetical |
| | Sauron p399 | 0.00003 | Hypothetical |
| NY12 p399 | Sauron p401 | 1E-83 | Hypothetical |
| | Sauron p403 | 0.00000002 | Hypothetical |
| | Sauron p391 | 0.0000004 | Hypothetical |
| | Sauron p398 | 0.0002 | Hypothetical |
| | Sauron p390 | 0.0003 | Hypothetical |
| NY12 p400 | Sauron p402 | 1E-88 | Hypothetical |
| | Sauron p393 | 0.000002 | Hypothetical |
| | Sauron p400 | 0.00008 | Hypothetical |
| | Sauron p396 | 0.0002 | Hypothetical |
| | Sauron p345 | 0.0003 | Hypothetical |
| NY12 p401 | Sauron p403 | 2E-76 | Hypothetical |
| | Sauron p394 | 5E-10 | Hypothetical |
| | Sauron p393 | 0.000000003 | Hypothetical |
| | Sauron p401 | 0.000000008 | Hypothetical |
| | Sauron p395 | 0.000002 | Hypothetical |
| | Sauron p390 | 0.000003 | Hypothetical |
| | Sauron p392 | 0.00003 | Hypothetical |
| | Sauron p398 | 0.00006 | Hypothetical |
| | Sauron p396 | 0.00006 | Hypothetical |
| | Sauron p391 | 0.0002 | Hypothetical |
| NY12 p402 | Sauron p404 | 5E-33 | Hypothetical |
| NY12 p403 | Sauron p405 | 2E-108 | Hypothetical |
| NY12 p404 | Sauron p406 | 9E-172 | Hypothetical |
| NY12 p405 | Sauron p407 | 7E-78 | Hypothetical |
| NY12 p406 | Sauron p408 | 2E-75 | Hypothetical |
| NY12 p407 | Sauron p409 | 9E-50 | Hypothetical |
| NY12 p408 | Sauron p410 | 2E-39 | Hypothetical |

| Gene | Match to Sauron | E Value | Putative Function |
|---|---|---|---|
| NY12 p409 | Sauron p411 | 3E-73 | Hypothetical |
| NY12 p410 | Sauron p412 | 1E-54 | Hypothetical |
| NY12 p411 | Sauron p413 | 6E-51 | Bacteriophage-Associated Superinfection Exclusion Protein |
| | Sauron p414 | 2E-10 | Bacteriophage-Associated Superinfection Exclusion Protein |
| NY12 p412 | Sauron p414 | 3E-40 | Bacteriophage-Associated Superinfection Exclusion Protein |
| | Sauron p413 | 9E-11 | Bacteriophage-Associated Superinfection Exclusion Protein |
| NY12 p413 | Sauron p415 | 2E-74 | Hypothetical |
| NY12 p414 | Sauron p416 | 2E-74 | Hypothetical |
| NY12 p415 | Sauron p417 | 2E-133 | Hypothetical |
| NY12 p416 | Sauron p418 | 1E-35 | Hypothetical |
| NY12 p417 | Sauron p419 | 0 | Hypothetical |
| NY12 p418 | Sauron p420 | 1E-130 | Hypothetical |
| NY12 p419 | Sauron p421 | 0 | Hypothetical |
| NY12 p420 | Sauron p422 | 2E-36 | Hypothetical |
| NY12 p421 | Sauron p423 | 2E-79 | Hypothetical |
| NY12 p422 | Sauron p424 | 0 | Hypothetical |
| NY12 p423 | Sauron p425 | 2E-146 | Hypothetical |
| NY12 p424 | Sauron p426 | 5E-74 | Hypothetical |
| NY12 p425 | Sauron p427 | 2E-127 | Hypothetical |
| NY12 p426 | Sauron p428 | 2E-97 | Hypothetical |
| NY12 p427 | Sauron p429 | 1E-108 | Hypothetical |
| NY12 p428 | Sauron p430 | 3E-43 | Hypothetical |
| NY12 p429 | Sauron p431 | 5E-122 | Hypothetical |
| NY12 p430 | Sauron p432 | 9E-35 | Hypothetical |
| NY12 p431 | Sauron p433 | 1E-57 | Hypothetical |
| NY12 p432 | Sauron p434 | 2E-84 | Hypothetical |
| NY12 p433 | Sauron p435 | 2E-83 | Hypothetical |
| NY12 p434 | Sauron p436 | 8E-67 | Hypothetical |
| NY12 p435 | Sauron p437 | 0 | Hypothetical |
| NY12 p436 | Sauron p438 | 1E-116 | (p)ppGpp Synthetase |
| NY12 p437 | Sauron p439 | 2E-144 | Hypothetical |
| NY12 p438 | Sauron p440 | 2E-71 | Hypothetical |
| NY12 p439 | Sauron p441 | 2E-30 | Hypothetical |
| NY12 p440 | Sauron p442 | 4E-63 | Hypothetical |
| NY12 p441 | Sauron p443 | 1E-95 | Hypothetical |
| NY12 p442 | Sauron p444 | 3E-118 | Hypothetical |
| NY12 p443 | Sauron p445 | 6E-48 | Hypothetical |
| NY12 p444 | Sauron p446 | 8E-126 | Hypothetical |
| NY12 p445 | Sauron p443 | 4E-14 | Hypothetical |

Table 2: Sauron Annotation Table

| Gene | Match to NY12 | E Value | Putative Function |
|---|---|---|---|
| Sauron p001 | NY12 p001 | 1E-31 | Hypothetical |
| Sauron p002 | NY12 p002 | 8E-41 | Hypothetical |
| Sauron p003 | NY12 p003 | 4E-25 | Hypothetical |
| Sauron p004 | None | n/a | Hypothetical |
| Sauron p005 | NY12 p004 | 1E-56 | Hypothetical |
| Sauron p006 | NY12 p005 | 3E-23 | Hypothetical |
| Sauron p007 | NY12 p006 | 2E-23 | Hypothetical |
| Sauron p008 | NY12 p007 | 2E-29 | Hypothetical |
| Sauron p009 | NY12 p008 | 1E-34 | Hypothetical |
| Sauron p010 | NY12 p009 | 8E-12 | Hypothetical |
| Sauron p011 | NY12 p010 | 2E-53 | Hypothetical |
| Sauron p012 | NY12 p011 | 1E-30 | Hypothetical |
| Sauron p013 | NY12 p013 | 4E-34 | Hypothetical |
| Sauron p014 | NY12 p014 | 5E-35 | Hypothetical |
| Sauron p015 | NY12 p015 | 1E-26 | Hypothetical |
| Sauron p016 | NY12 p016 | 1E-108 | Hypothetical |
| Sauron p017 | NY12 p017 | 2E-35 | Hypothetical |
| Sauron p018 | NY12 p018 | 5E-29 | Hypothetical |
| Sauron p019 | NY12 p019 | 9E-39 | Hypothetical |
| Sauron p020 | NY12 p020 | 4E-26 | Hypothetical |
| Sauron p021 | NY12 p021 | 6E-51 | Hypothetical |
| Sauron p022 | None | n/a | Hypothetical |
| Sauron p023 | NY12 p022 | 4E-54 | Hypothetical |
| Sauron p024 | NY12 p023 | 8E-79 | Hypothetical |
| Sauron p025 | NY12 p024 | 3E-44 | Hypothetical |
| Sauron p026 | NY12 p025 | 2E-35 | Hypothetical |
| Sauron p027 | NY12 p026 | 2E-139 | Hypothetical |
| Sauron p028 | NY12 p027 | 2E-39 | Hypothetical |
| Sauron p029 | NY12 p028 | 1E-80 | Hypothetical |
| Sauron p030 | NY12 p029 | 1E-40 | Hypothetical |
| Sauron p031 | NY12 p030 | 3E-38 | Hypothetical |
| Sauron p032 | NY12 p031 | 1E-29 | Hypothetical |
| Sauron p033 | NY12 p033 | 7E-44 | Hypothetical |
| Sauron p034 | None | n/a | Hypothetical |
| Sauron p035 | NY12 p034 | 3E-20 | Hypothetical |
| Sauron p036 | NY12 p035 | 1E-176 | Hypothetical |
| Sauron p037 | NY12 p037 | 3E-67 | Hypothetical |
| Sauron p038 | NY12 p038 | 1E-44 | Hypothetical |
| Sauron p039 | NY12 p039 | 9E-101 | Hypothetical |
| Sauron p040 | NY12 p040 | 3E-100 | Hypothetical |

| Gene | Match to NY12 | E Value | Putative Function |
|---|---|---|---|
| Sauron p041 | None | n/a | Hypothetical |
| Sauron p042 | NY12 p041 | 1E-158 | Hypothetical |
| Sauron p043 | NY12 p042 | 5E-122 | Hypothetical |
| Sauron p044 | NY12 p043 | 4E-32 | Hypothetical |
| Sauron p045 | NY12 p044 | 2E-87 | Hypothetical |
| Sauron p046 | NY12 p045 | 2E-18 | Hypothetical |
| Sauron p047 | NY12 p046 | 1E-119 | Hypothetical |
| Sauron p048 | NY12 p047 | 2E-52 | Hypothetical |
| Sauron p049 | NY12 p048 | 1E-21 | Hypothetical |
| Sauron p050 | NY12 p049 | 1E-22 | Hypothetical |
| Sauron p051 | NY12 p050 | 1E-85 | Hypothetical |
| Sauron p052 | NY12 p051 | 1E-53 | Hypothetical |
| Sauron p053 | NY12 p052 | 6E-24 | Hypothetical |
| Sauron p054 | NY12 p053 | 4E-46 | Hypothetical |
| Sauron p055 | NY12 p054 | 8E-94 | Hypothetical |
| Sauron p056 | NY12 p056 | 1E-94 | Hypothetical |
| | Ny12 p055 | 2E-35 | Hypothetical |
| Sauron p057 | NY12 p057 | 1E-66 | Hypothetical |
| Sauron p058 | NY12 p058 | 3E-76 | Hypothetical |
| Sauron p059 | NY12 p059 | 1E-69 | Hypothetical |
| Sauron p060 | NY12 p060 | 4E-67 | Hypothetical |
| Sauron p061 | NY12 p061 | 9E-66 | Hypothetical |
| Sauron p062 | NY12 p062 | 2E-54 | Hypothetical |
| Sauron p063 | NY12 p063 | 4E-78 | Hypothetical |
| Sauron p064 | NY12 p064 | 2E-97 | Hypothetical |
| Sauron p065 | NY12 p065 | 9E-107 | Hypothetical |
| Sauron p066 | NY12 p066 | 9E-87 | Hypothetical |
| Sauron p067 | NY12 p067 | 1E-68 | Hypothetical |
| Sauron p068 | NY12 p068 | 1E-63 | Hypothetical |
| Sauron p069 | None | n/a | Hypothetical |
| Sauron p070 | NY12 p070 | 0E+00 | Homing Endonuclease (GIY-YIG) |
| Sauron p071 | NY12 p071 | 4E-54 | Hypothetical |
| Sauron p072 | NY12 p072 | 2E-61 | Hypothetical |
| Sauron p073 | NY12 p073 | 1E-27 | Hypothetical |
| Sauron p074 | NY12 p074 | 1E-144 | Hypothetical |
| Sauron p075 | NY12 p075 | 0E+00 | Hypothetical |
| Sauron p076 | NY12 p076 | 8E-98 | Tail Tube Protein |
| Sauron p077 | NY12 p077 | 2E-64 | Hypothetical |
| Sauron p078 | NY12 p078 | 0E+00 | Tail Sheath Protein |
| | NY12 p262 | 4E-08 | Baseplate Wedge Subunit |
| Sauron p079 | NY12 p079 | 2E-44 | Hypothetical |
| Sauron p080 | NY12 p080 | 4E-138 | Hypothetical |
| Sauron p081 | NY12 p081 | 4E-61 | Hypothetical |

| Gene | Match to NY12 | E Value | Putative Function |
|---|---|---|---|
| Sauron p082 | NY12 p082 | 0E+00 | Hypothetical |
| Sauron p083 | NY12 p083 | 3E-135 | Hypothetical |
| Sauron p084 | NY12 p084 | 0E+00 | Hypothetical |
| Sauron p085 | NY12 p085 | 1E-179 | Hypothetical |
| Sauron p086 | NY12 p086 | 1E-74 | Hypothetical |
| Sauron p087 | NY12 p087 | 8E-59 | Hypothetical |
| Sauron p088 | NY12 p088 | 0E+00 | SNF2-like Helicase |
| Sauron p089 | NY12 p089 | 6E-141 | Hypothetical |
| Sauron p090 | NY12 p090 | 6E-84 | Hypothetical |
| Sauron p091 | NY12 p092 | 5E-76 | Hypothetical |
| Sauron p092 | NY12 p093 | 0E+00 | Hypothetical |
| Sauron p093 | NY12 p094 | 3E-69 | Hypothetical |
| Sauron p094 | NY12 p095 | 4E-164 | Hypothetical |
| Sauron p095 | NY12 p096 | 0E+00 | Hypothetical |
| Sauron p096 | NY12 p097 | 1E-69 | Hypothetical |
| Sauron p097 | NY12 p098 | 3E-87 | Cytidine/Deoxycytidine Deaminase |
| Sauron p098 | NY12 p099 | 5E-38 | Hypothetical |
| Sauron p099 | NY12 p100 | 2E-109 | NUDIX Hydrolase Domain |
| Sauron p100 | NY12 p101 | 5E-173 | Hypothetical |
| Sauron p101 | NY12 p102 | 1E-86 | Hypothetical |
| Sauron p102 | NY12 p103 | 2E-51 | Hypothetical |
| Sauron p103 | NY12 p104 | 3E-30 | Hypothetical |
| Sauron p104 | NY12 p105 | 4E-38 | Hypothetical |
| Sauron p105 | NY12 p106 | 1E-105 | Hypothetical |
| Sauron p106 | NY12 p107 | 3E-26 | Hypothetical |
| Sauron p107 | NY12 p108 | 6E-38 | Hypothetical |
| Sauron p108 | NY12 p109 | 2E-127 | Hypothetical |
| Sauron p109 | NY12 p110 | 6E-175 | Kelch-motif Containing Protein |
| Sauron p110 | NY12 p111 | 6E-45 | Hypothetical |
| Sauron p111 | NY12 p112 | 1E-110 | Hypothetical |
| Sauron p112 | NY12 p113 | 0E+00 | Nicotinate Phosphoribosyltransferase |
| Sauron p113 | NY12 p114 | 1E-58 | Hypothetical |
| Sauron p114 | NY12 p115 | 0E+00 | Putative Cytidyltransferase |
| Sauron p115 | NY12 p116 | 4E-39 | Hypothetical |
| Sauron p116 | NY12 p117 | 0E+00 | NAD-dependent DNA Ligase |
| Sauron p117 | NY12 p118 | 4E-32 | Hypothetical |
| Sauron p118 | NY12 p119 | 1E-44 | Acyl Carrier Protein-like |
| Sauron p119 | NY12 p120 | 6E-86 | Hypothetical |
| Sauron p120 | NY12 p121 | 8E-78 | Hypothetical |
| Sauron p121 | NY12 p122 | 5E-132 | Hypothetical |
| Sauron p122 | NY12 p123 | 4E-76 | Hypothetical |
| Sauron p123 | NY12 p124 | 6E-30 | Hypothetical |
| Sauron p124 | NY12 p125 | 2E-66 | Hypothetical |

| Gene | Match to NY12 | E Value | Putative Function |
|---|---|---|---|
| Sauron p125 | NY12 p126 | 0E+00 | Hypothetical |
| Sauron p126 | NY12 p127 | 4E-117 | Putative Phosphatase |
| Sauron p127 | NY12 p128 | 2E-83 | HNH Endonuclease |
| Sauron p128 | NY12 p129 | 7E-67 | Hypothetical |
| Sauron p129 | NY12 p130 | 9E-88 | Aspartyl/glutamyl-tRNA Amidotransferase Subunit B-like |
| Sauron p130 | NY12 p131 | 0E+00 | RtcB-like Protein |
| Sauron p131 | NY12 p132 | 1E-80 | NUDIX Hydrolase |
| Sauron p132 | NY12 p133 | 3E-56 | Hypothetical |
| Sauron p133 | NY12 p134 | 1E-46 | Hypothetical |
| Sauron p134 | NY12 p135 | 2E-46 | Hypothetical |
| Sauron p135 | NY12 p136 | 4E-38 | Hypothetical |
| Sauron p136 | NY12 p137 | 9E-100 | Hypothetical |
| Sauron p137 | NY12 p138 | 3E-56 | Hypothetical |
| Sauron p138 | None | n/a | Hypothetical |
| Sauron p139 | NY12 p139 | 5E-40 | Hypothetical |
| Sauron p140 | NY12 p140 | 2E-87 | Hypothetical |
| Sauron p141 | NY12 p141 | 2E-66 | Hypothetical |
| Sauron p142 | NY12 p142 | 9E-28 | Hypothetical |
| Sauron p143 | NY12 p143 | 7E-38 | Hypothetical |
| Sauron p144 | NY12 p144 | 7E-41 | Hypothetical |
| Sauron p145 | NY12 p145 | 2E-49 | Hypothetical |
| Sauron p146 | NY12 p146 | 2E-78 | Hypothetical |
| Sauron p147 | NY12 p147 | 7E-52 | Hypothetical |
| Sauron p148 | None | n/a | Hypothetical |
| Sauron p149 | NY12 p148 | 4E-43 | Hypothetical |
| | NY12 p149 | 7E-09 | Hypothetical |
| Sauron p150 | NY12 p149 | 9E-39 | Hypothetical |
| | NY12 p148 | 1E-10 | Hypothetical |
| Sauron p151 | NY12 p150 | 2E-61 | Hypothetical |
| Sauron p152 | NY12 p151 | 4E-86 | Hypothetical |
| Sauron p153 | NY12 p153 | 7E-57 | Hypothetical |
| Sauron p154 | NY12 p154 | 6E-83 | Hypothetical |
| Sauron p155 | NY12 p155 | 2E-35 | Hypothetical |
| Sauron p156 | NY12 p156 | 3E-41 | Hypothetical |
| Sauron p157 | NY12 p157 | 1E-44 | Hypothetical |
| Sauron p158 | NY12 p158 | 2E-70 | Hypothetical |
| Sauron p159 | NY12 p159 | 0E+00 | Hypothetical |
| Sauron p160 | NY12 p160 | 0E+00 | Putative RNA Ligase |
| Sauron p161 | NY12 p161 | 2E-140 | Hypothetical |
| Sauron p162 | NY12 p162 | 4E-63 | Hypothetical |
| Sauron p163 | NY12 p163 | 3E-88 | Hypothetical |
| Sauron p164 | NY12 p165 | 4E-99 | Hypothetical |
| Sauron p165 | NY12 p166 | 0E+00 | Hypothetical |

| Gene | Match to NY12 | E Value | Putative Function |
|---|---|---|---|
| Sauron p166 | NY12 p167 | 1E-17 | Hypothetical |
| Sauron p167 | NY12 p168 | 0E+00 | Hypothetical |
| Sauron p168 | NY12 p169 | 0E+00 | Type IIA DNA Topoisomerase, GyrA-like |
| Sauron p169 | NY12 p170 | 0E+00 | Type IIA DNA Topoisomerase, GyrB-like |
| Sauron p170 | NY12 p172 | 7E-158 | Hypothetical |
| Sauron p171 | NY12 p173 | 1E-57 | Hypothetical |
| Sauron p172 | NY12 p174 | 2E-64 | Hypothetical |
| Sauron p173 | NY12 p175 | 1E-122 | Hypothetical |
| Sauron p174 | NY12 p176 | 2E-144 | Hypothetical |
| Sauron p175 | NY12 p177 | 6E-49 | Hypothetical |
| Sauron p176 | NY12 p178 | 3E-35 | Hypothetical |
| Sauron p177 | NY12 p179 | 6E-57 | Hypothetical |
| Sauron p178 | NY12 p180 | 1E-96 | Hypothetical |
| Sauron p179 | NY12 p181 | 3E-34 | Hypothetical |
| Sauron p180 | NY12 p182 | 2E-102 | Hypothetical |
| Sauron p181 | NY12 p183 | 3E-71 | Hypothetical |
| Sauron p182 | NY12 p184 | 2E-18 | Hypothetical |
| Sauron p183 | NY12 p185 | 4E-64 | Hypothetical |
| Sauron p184 | NY12 p186 | 1E-53 | Hypothetical |
| Sauron p185 | NY12 p187 | 2E-98 | Hypothetical |
| Sauron p186 | NY12 p188 | 2E-140 | Hypothetical |
| Sauron p187 | NY12 p189 | 3E-50 | Hypothetical |
| Sauron p188 | NY12 p190 | 3E-63 | Hypothetical |
| Sauron p189 | None | n/a | Hypothetical |
| Sauron p190 | NY12 p191 | 2E-67 | Hypothetical |
| Sauron p191 | NY12 p192 | 0E+00 | Recombination Endonuclease-like Protein |
| Sauron p192 | NY12 p193 | 5E-105 | Hypothetical |
| Sauron p193 | NY12 p194 | 0E+00 | DEAD Type Helicase |
| | NY12 p381 | 4E-106 | Hypothetical |
| Sauron p194 | None | n/a | Hypothetical |
| Sauron p195 | NY12 p196 | 2E-50 | Hypothetical |
| Sauron p196 | NY12 p197 | 4E-65 | Hypothetical |
| Sauron p197 | NY12 p198 | 2E-56 | Hypothetical |
| Sauron p198 | NY12 p199 | 9E-20 | Hypothetical |
| Sauron p199 | NY12 p200 | 4E-41 | Hypothetical |
| Sauron p200 | NY12 p201 | 2E-49 | Hypothetical |
| Sauron p201 | NY12 p202 | 2E-37 | Hypothetical |
| Sauron p202 | NY12 p203 | 1E-82 | Hypothetical |
| Sauron p203 | NY12 p204 | 1E-76 | Hypothetical |
| Sauron p204 | NY12 p205 | 3E-46 | Hypothetical |
| Sauron p205 | None | n/a | HNH Endonuclease |
| Sauron p206 | None | n/a | Hypothetical |
| Sauron p207 | NY12 p206 | 6E-64 | Hypothetical |

| Gene | Match to NY12 | E Value | Putative Function |
|---|---|---|---|
| Sauron p208 | NY12 p207 | 1E-35 | Hypothetical |
| Sauron p209 | NY12 p208 | 7E-63 | Hypothetical |
| Sauron p210 | NY12 p209 | 1E-81 | Hypothetical |
| | NY12 p249 | 2E-13 | Hypothetical |
| Sauron p211 | NY12 p210 | 1E-60 | Hypothetical |
| Sauron p212 | NY12 p211 | 3E-40 | GroES-like Protein |
| Sauron p213 | NY12 p212 | 3E-58 | Thioredoxin |
| Sauron p214 | NY12 p213 | 6E-32 | Hypothetical |
| Sauron p215 | NY12 p214 | 3E-62 | Hypothetical |
| Sauron p216 | None | n/a | Hypothetical |
| Sauron p217 | NY12 p215 | 1E-30 | Hypothetical |
| Sauron p218 | NY12 p216 | 0E+00 | ATP-binding Protein |
| Sauron p219 | NY12 p217 | 1E-166 | Endodeoxyribonuclease |
| Sauron p220 | NY12 p218 | 1E-41 | Hypothetical |
| Sauron p221 | NY12 p219 | 5E-66 | Hypothetical |
| Sauron p222 | NY12 p220 | 2E-43 | Hypothetical |
| Sauron p223 | NY12 p221 | 3E-138 | Metal Dependent Phosphohydrolase-like Protein |
| Sauron p224 | None | n/a | HNH Endonuclease |
| Sauron p225 | NY12 p222 | 0E+00 | DNA Polymerase I |
| Sauron p226 | NY12 p223 | 1E-79 | Hypothetical |
| Sauron p227 | NY12 p224 | 7E-131 | Hypothetical |
| Sauron p228 | NY12 p225 | 0E+00 | DNA Primase |
| Sauron p229 | NY12 p226 | 3E-74 | Putative i-spanin |
| Sauron p230 | NY12 p227 | 5E-57 | Putative o-spanin |
| Sauron p231 | NY12 p228 | 0E+00 | Hypothetical |
| | NY12 p249 | 2E-06 | Hypothetical |
| Sauron p232 | NY12 p230 | 4E-169 | Hypothetical |
| Sauron p233 | NY12 p231 | 4E-65 | Hypothetical |
| Sauron p234 | NY12 p232 | 6E-89 | Hypothetical |
| Sauron p235 | NY12 p233 | 3E-67 | Hypothetical |
| Sauron p236 | NY12 p234 | 1E-87 | Hypothetical |
| Sauron p237 | NY12 p235 | 2E-74 | Hypothetical |
| Sauron p238 | NY12 p237 | 2E-124 | Thymidylate Synthase |
| Sauron p239 | NY12 p238 | 1E-130 | Hypothetical |
| Sauron p240 | NY12 p239 | 0E+00 | Hypothetical |
| Sauron p241 | NY12 p240 | 7E-63 | Hypothetical |
| Sauron p242 | NY12 p241 | 1E-163 | Hypothetical |
| Sauron p243 | NY12 p242 | 0E+00 | RecA-like Recombinase |
| Sauron p244 | NY12 p243 | 2E-135 | Hypothetical |
| Sauron p245 | NY12 p244 | 0E+00 | Terminase |
| Sauron p246 | NY12 p245 | 2E-124 | RuvC Resolvase-like Protein |
| Sauron p247 | NY12 p246 | 2E-42 | Hypothetical |
| Sauron p248 | NY12 p247 | 1E-164 | Hypothetical |

| Gene | Match to NY12 | E Value | Putative Function |
|---|---|---|---|
| Sauron p249 | None | n/a | Hypothetical |
| Sauron p250 | NY12 p248 | 2E-90 | Hypothetical |
| Sauron p251 | NY12 p249 | 0E+00 | Hypothetical |
| | NY12 p209 | 4E-12 | Hypothetical |
| Sauron p252 | NY12 p250 | 4E-85 | Hypothetical |
| Sauron p253 | NY12 p251 | 1E-49 | Hypothetical |
| Sauron p254 | NY12 p164 | 3E-20 | Homing Endonuclease |
| | NY12 P229 | 2E-09 | Homing Endonuclease |
| Sauron p255 | NY12 p252 | 1E-159 | Hypothetical |
| Sauron p256 | NY12 p253 | 0E+00 | Hypothetical |
| Sauron p257 | NY12 p254 | 2E-26 | Hypothetical |
| Sauron p258 | NY12 p255 | 0E+00 | Hypothetical |
| Sauron p259 | NY12 p256 | 0E+00 | Tail Protein |
| Sauron p260 | NY12 p257 | 0E+00 | Hypothetical |
| Sauron p261 | NY12 p258 | 7E-67 | Hypothetical |
| Sauron p262 | NY12 p259 | 0E+00 | Hypothetical |
| Sauron p263 | NY12 p260 | 4E-158 | Hypothetical |
| Sauron p264 | NY12 p261 | 5E-82 | Baseplate Wedge Subunit |
| Sauron p265 | NY12 p262 | 0E+00 | Baseplate Wedge Subunit |
| | NY12 p078 | 3E-08 | Tail Sheath Protein |
| Sauron p266 | NY12 p263 | 7E-159 | Hypothetical |
| Sauron p267 | NY12 p264 | 0E+00 | Phage Tail Collar Protein |
| | NY12 p287 | 9E-15 | Phage Tail Collar Protein |
| Sauron p268 | NY12 p265 | 4E-104 | Hypothetical |
| Sauron p269 | NY12 p266 | 4E-101 | Hypothetical |
| Sauron p270 | NY12 p267 | 4E-40 | Hypothetical |
| Sauron p271 | NY12 p268 | 7E-72 | Hypothetical |
| Sauron p272 | NY12 p269 | 0E+00 | Hypothetical |
| Sauron p273 | NY12 p270 | 0E+00 | Hypothetical |
| | NY12 p279 | 1E-06 | Hypothetical |
| Sauron p274 | NY12 p271 | 0E+00 | Hypothetical |
| | NY12 p281 | 2E-17 | Hypothetical |
| | NY12 p287 | 1E-12 | Phage Tail Collar Protein |
| | NY12 p280 | 2E-07 | Putative Long Tail Fiber Protein |
| | NY12 p280 | 5E-06 | Putative Long Tail Fiber Protein |
| Sauron p275 | NY12 p272 | 7E-87 | Hypothetical |
| Sauron p276 | NY12 p275 | 7E-93 | Hypothetical |
| Sauron p277 | NY12 p276 | 3E-52 | Hypothetical |
| Sauron p278 | NY12 p277 | 2E-66 | Hypothetical |
| Sauron p279 | NY12 p278 | 0E+00 | Hypothetical |
| Sauron p280 | NY12 p279 | 0E+00 | Hypothetical |
| | NY12 p270 | 1E-06 | Hypothetical |
| Sauron p281 | NY12 p280 | 0E+00 | Putative Long Tail Fiber Protein |

| Gene | Match to NY12 | E Value | Putative Function |
|---|---|---|---|
| | NY12 p287 | 2E-14 | Phage Tail Collar Protein |
| | NY12 p287 | 4E-11 | Phage Tail Collar Protein |
| | NY12 p287 | 2E-06 | Phage Tail Collar Protein |
| | NY12 p271 | 1E-08 | Hypothetical |
| | NY12 p271 | 1E-06 | Hypothetical |
| | NY12 p273 | 1E-07 | Hypothetical |
| | NY12 p272 | 2E-06 | Putative Tail Fiber Protein |
| Sauron p282 | NY12 p281 | 0E+00 | Hypothetical |
| | NY12 p271 | 3E-18 | Hypothetical |
| | NY12 p274 | 2E-08 | Hypothetical |
| Sauron p283 | NY12 p282 | 2E-128 | Putative Endolysin (GH19) |
| Sauron p284 | NY12 p283 | 1E-89 | Putative Antiholin |
| Sauron p285 | NY12 p284 | 7E-67 | Putative Type 1 Holin |
| Sauron p286 | NY12 p285 | 3E-54 | Hypothetical |
| Sauron p287 | NY12 p286 | 0E+00 | 5'-3' Exonuclease |
| Sauron p288 | NY12 p287 | 0E+00 | Phage Tail Collar Protein |
| | NY12 p264 | 3E-14 | Phage Tail Collar Protein |
| | NY12 p280 | 1E-13 | Putative Long Tail Fiber Protein |
| | NY12 p280 | 7E-11 | Putative Long Tail Fiber Protein |
| | NY12 p280 | 2E-06 | Putative Long Tail Fiber Protein |
| | NY12 p271 | 1E-12 | Hypothetical |
| Sauron p289 | NY12 p288 | 1E-163 | Hypothetical |
| Sauron p290 | NY12 p289 | 4E-38 | Hypothetical |
| Sauron p291 | None | n/a | NrdA-like Protein |
| Sauron p292 | NY12 p291 | 7E-18 | Hypothetical |
| | NY12 p082 | 6E-06 | Putative Capsid Protein |
| Sauron p293 | NY12 p292 | 4E-32 | Hypothetical |
| Sauron p294 | NY12 p293 | 6E-43 | Hypothetical |
| Sauron p295 | NY12 p294 | 5E-33 | Hypothetical |
| Sauron p296 | NY12 p295 | 0E+00 | DNA Polymerase III-like Protein |
| Sauron p297 | NY12 p296 | 0E+00 | ATPase Domain Containing Protein |
| Sauron p298 | NY12 p297 | 1E-140 | Hypothetical |
| Sauron p299 | NY12 p298 | 4E-67 | Hypothetical |
| Sauron p300 | NY12 p299 | 3E-166 | Hypothetical |
| Sauron p301 | NY12 p300 | 4E-75 | Hypothetical |
| Sauron p302 | NY12 p301 | 0E+00 | DNA Polymerase III Beta Subunit-like |
| Sauron p303 | NY12 p302 | 2E-77 | Hypothetical |
| Sauron p304 | NY12 p303 | 5E-25 | Hypothetical |
| Sauron p305 | NY12 p304 | 1E-102 | Hypothetical |
| Sauron p306 | NY12 p305 | 4E-38 | Hypothetical |
| Sauron p307 | NY12 p306 | 5E-33 | Hypothetical |
| Sauron p308 | NY12 p307 | 8E-71 | Hypothetical |
| Sauron p309 | NY12 p308 | 0E+00 | ATP-Dependent Helicase |

| Gene | Match to NY12 | E Value | Putative Function |
|---|---|---|---|
| Sauron p310 | NY12 p309 | 1E-68 | Hypothetical |
| Sauron p311 | NY12 p310 | 2E-153 | Hypothetical |
| Sauron p312 | NY12 p311 | 2E-64 | Hypothetical |
| Sauron p313 | NY12 p312 | 2E-50 | Hypothetical |
| Sauron p314 | NY12 p313 | 0E+00 | Hypothetical |
| Sauron p315 | None | n/a | Hypothetical |
| Sauron p316 | NY12 p314 | 5E-69 | Hypothetical |
| Sauron p317 | NY12 p315 | 1E-30 | Hypothetical |
| Sauron p318 | NY12 p316 | 0E+00 | Replicative DNA Helicase |
| Sauron p319 | None | n/a | Hypothetical |
| Sauron p320 | NY12 p318 | 2E-19 | Hypothetical |
| Sauron p321 | NY12 p319 | 8E-69 | Hypothetical |
| Sauron p322 | NY12 p320 | 4E-09 | Hypothetical |
| Sauron p323 | NY12 p321 | 0E+00 | Hypothetical |
| Sauron p324 | NY12 p322 | 1E-38 | Hypothetical |
| Sauron p325 | NY12 p339 | 6E-12 | Hypothetical |
| | NY12 p339 | 4E-11 | Hypothetical |
| Sauron p326 | NY12 p324 | 1E-62 | Hypothetical |
| Sauron p327 | NY12 p325 | 8E-45 | Hypothetical |
| Sauron p328 | NY12 p326 | 1E-36 | Hypothetical |
| Sauron p329 | NY12 p327 | 4E-125 | Hypothetical |
| Sauron p330 | NY12 p328 | 1E-80 | Hypothetical |
| Sauron p331 | NY12 p329 | 2E-36 | Hypothetical |
| Sauron p332 | NY12 p330 | 1E-18 | Hypothetical |
| Sauron p333 | NY12 p331 | 1E-33 | Hypothetical |
| Sauron p334 | NY12 p332 | 3E-116 | tRNA His Guanylyltransferase Thg1 |
| Sauron p335 | NY12 p333 | 5E-24 | Hypothetical |
| Sauron p336 | NY12 p334 | 2E-45 | Hypothetical |
| Sauron p337 | NY12 p335 | 3E-37 | Hypothetical |
| Sauron p338 | NY12 p336 | 3E-36 | Hypothetical |
| Sauron p339 | NY12 p337 | 1E-119 | Hypothetical |
| Sauron p340 | NY12 p338 | 7E-29 | Hypothetical |
| Sauron p341 | NY12 p339 | 0E+00 | Hypothetical |
| Sauron p342 | NY12 p340 | 2E-26 | Hypothetical |
| Sauron p343 | NY12 p341 | 4E-35 | Hypothetical |
| Sauron p344 | NY12 p343 | 3E-07 | Hypothetical |
| Sauron p345 | NY12 p342 | 3E-55 | Hypothetical |
| Sauron p346 | NY12 p343 | 5E-28 | Hypothetical |
| Sauron p347 | NY12 p344 | 3E-38 | Hypothetical |
| Sauron p348 | NY12 p345 | 9E-37 | Hypothetical |
| Sauron p349 | NY12 p346 | 2E-68 | Hypothetical |
| Sauron p350 | NY12 p347 | 2E-90 | Hypothetical |
| Sauron p351 | NY12 p348 | 3E-34 | Hypothetical |

| Gene | Match to NY12 | E Value | Putative Function |
|---|---|---|---|
| Sauron p352 | NY12 p349 | 1E-52 | Hypothetical |
| Sauron p353 | NY12 p350 | 2E-54 | Hypothetical |
| Sauron p354 | NY12 p351 | 2E-22 | Hypothetical |
| Sauron p355 | NY12 p352 | 1E-57 | Hypothetical |
| Sauron p356 | NY12 p353 | 2E-85 | Hypothetical |
| Sauron p357 | NY12 p354 | 6E-96 | Hypothetical |
| Sauron p358 | NY12 p355 | 3E-27 | Hypothetical |
| Sauron p359 | NY12 p356 | 5E-40 | Hypothetical |
| Sauron p360 | NY12 p357 | 8E-41 | Hypothetical |
| Sauron p361 | NY12 p358 | 2E-78 | Hypothetical |
| Sauron p362 | NY12 p359 | 3E-39 | Hypothetical |
| Sauron p363 | NY12 p360 | 2E-70 | Hypothetical |
| Sauron p364 | NY12 p361 | 4E-42 | Hypothetical |
| Sauron p365 | NY12 p362 | 3E-54 | Hypothetical |
| Sauron p366 | NY12 p363 | 3E-77 | Hypothetical |
| Sauron p367 | NY12 p364 | 2E-36 | Hypothetical |
| Sauron p368 | NY12 p365 | 6E-43 | Hypothetical |
| Sauron p369 | NY12 p366 | 3E-52 | Hypothetical |
| Sauron p370 | NY12 p367 | 1E-52 | Hypothetical |
| Sauron p371 | NY12 p368 | 9E-42 | Hypothetical |
| Sauron p372 | NY12 p369 | 8E-49 | Hypothetical |
| Sauron p373 | NY12 p370 | 0E+00 | T4 RnlA-like RNA ligase and Tail Fiber Attachment Catalyst |
| Sauron p374 | NY12 p371 | 1E-63 | Hypothetical |
| Sauron p375 | NY12 p372 | 3E-11 | Hypothetical |
| Sauron p376 | NY12 p373 | 4E-43 | Hypothetical |
| Sauron p377 | NY12 p374 | 7E-145 | Putative Nucleotidyltransferase |
| Sauron p378 | NY12 p375 | 1E-11 | Hypothetical |
| Sauron p379 | NY12 p376 | 1E-32 | Hypothetical |
| Sauron p380 | NY12 p377 | 2E-35 | Hypothetical |
| Sauron p381 | NY12 p378 | 4E-62 | Hypothetical |
| Sauron p382 | NY12 p379 | 4E-53 | Hypothetical |
| Sauron p383 | NY12 p380 | 6E-21 | Hypothetical |
| Sauron p384 | NY12 p381 | 0E+00 | Hypothetical |
| | NY12 p194 | 1E-106 | DEAD Type Helicase |
| Sauron p385 | NY12 p382 | 8E-37 | Hypothetical |
| Sauron p386 | NY12 p383 | 4E-80 | Hypothetical |
| Sauron p387 | NY12 p384 | 1E-39 | Hypothetical |
| Sauron p388 | NY12 p385 | 5E-83 | Hypothetical |
| Sauron p389 | NY12 p387 | 1E-65 | Hypothetical |
| | NY12 p386 | 3E-07 | Hypothetical |
| Sauron p390 | NY12 p388 | 5E-64 | Hypothetical |
| Sauron p391 | NY12 p389 | 8E-59 | Hypothetical |
| | NY12 p390 | 2E-07 | Hypothetical |

| Gene | Match to NY12 | E Value | Putative Function |
|---|---|---|---|
| | NY12 p391 | 2E-06 | Hypothetical |
| | NY12 p399 | 4E-06 | Hypothetical |
| Sauron p392 | NY12 p390 | 5E-71 | Hypothetical |
| | NY12 p391 | 2E-17 | Hypothetical |
| | NY12 p392 | 7E-12 | Hypothetical |
| | NY12 p389 | 3E-07 | Hypothetical |
| Sauron p393 | NY12 p391 | 2E-76 | Hypothetical |
| | NY12 p390 | 4E-15 | Hypothetical |
| | NY12 p392 | 3E-13 | Hypothetical |
| | NY12 p401 | 7E-08 | Hypothetical |
| | NY12 p389 | 2E-06 | Hypothetical |
| Sauron p394 | NY12 p392 | 2E-63 | Hypothetical |
| | NY12 p391 | 3E-14 | Hypothetical |
| | NY12 p390 | 5E-11 | Hypothetical |
| | NY12 p401 | 2E-08 | Hypothetical |
| | NY12 p389 | 9E-06 | Hypothetical |
| Sauron p395 | NY12 p393 | 6E-63 | Hypothetical |
| Sauron p396 | NY12 p394 | 9E-59 | Hypothetical |
| | NY12 p396 | 2E-08 | Hypothetical |
| Sauron p397 | NY12 p395 | 2E-41 | Hypothetical |
| Sauron p398 | NY12 p396 | 4E-57 | Hypothetical |
| | NY12 p394 | 6E-09 | Hypothetical |
| Sauron p399 | NY12 p397 | 9E-76 | Hypothetical |
| Sauron p400 | NY12 p398 | 4E-47 | Hypothetical |
| Sauron p401 | NY12 p399 | 5E-66 | Hypothetical |
| | NY12 p401 | 2E-07 | Hypothetical |
| | NY12 p389 | 1E-06 | Hypothetical |
| Sauron p402 | NY12 p400 | 5E-70 | Hypothetical |
| Sauron p403 | NY12 p401 | 2E-60 | Hypothetical |
| | NY12 p392 | 9E-08 | Hypothetical |
| | NY12 p391 | 2E-07 | Hypothetical |
| | NY12 p399 | 3E-07 | Hypothetical |
| Sauron p404 | NY12 p402 | 5E-26 | Hypothetical |
| Sauron p405 | NY12 p403 | 1E-85 | Hypothetical |
| Sauron p406 | NY12 p404 | 1E-136 | Hypothetical |
| Sauron p407 | NY12 p405 | 2E-61 | Hypothetical |
| Sauron p408 | NY12 p406 | 2E-59 | Hypothetical |
| Sauron p409 | NY12 p407 | 3E-39 | Hypothetical |
| Sauron p410 | NY12 p408 | 3E-31 | Hypothetical |
| Sauron p411 | NY12 p409 | 5E-58 | Hypothetical |
| Sauron p412 | NY12 p410 | 3E-43 | Hypothetical |
| Sauron p413 | NY12 p411 | 2E-40 | Bacteriophage-Associated Superinfection Exclusion Protein |
| | NY12 p412 | 6E-09 | Bacteriophage-Associated Superinfection Exclusion Protein |

| Gene | Match to NY12 | E Value | Putative Function |
|---|---|---|---|
| Sauron p414 | NY12 p412 | 7E-32 | Bacteriophage-Associated Superinfection Exclusion Protein |
| | NY12 p411 | 1E-08 | Bacteriophage-Associated Superinfection Exclusion Protein |
| Sauron p415 | NY12 p413 | 8E-59 | Hypothetical |
| Sauron p416 | NY12 p414 | 9E-59 | Hypothetical |
| Sauron p417 | NY12 p415 | 3E-105 | Hypothetical |
| Sauron p418 | NY12 p416 | 4E-28 | Hypothetical |
| Sauron p419 | NY12 p417 | 5E-146 | Hypothetical |
| Sauron p420 | NY12 p418 | 3E-103 | Hypothetical |
| Sauron p421 | NY12 p419 | 1E-163 | Hypothetical |
| Sauron p422 | NY12 p420 | 8E-29 | Hypothetical |
| Sauron p423 | NY12 p421 | 1E-62 | Hypothetical |
| Sauron p424 | NY12 p422 | 0E+00 | Hypothetical |
| Sauron p425 | NY12 p423 | 6E-116 | Hypothetical |
| Sauron p426 | NY12 p424 | 2E-58 | Hypothetical |
| Sauron p427 | NY12 p425 | 1E-100 | Hypothetical |
| Sauron p428 | NY12 p426 | 5E-77 | Hypothetical |
| Sauron p429 | NY12 p427 | 8E-86 | Hypothetical |
| Sauron p430 | NY12 p428 | 4E-34 | Hypothetical |
| Sauron p431 | NY12 p429 | 3E-96 | Hypothetical |
| Sauron p432 | NY12 p430 | 2E-27 | Hypothetical |
| Sauron p433 | NY12 p431 | 6E-46 | Hypothetical |
| Sauron p434 | NY12 p432 | 1E-66 | Hypothetical |
| Sauron p435 | NY12 p433 | 7E-66 | Hypothetical |
| Sauron p436 | NY12 p434 | 6E-53 | Hypothetical |
| Sauron p437 | NY12 p435 | 0E+00 | Hypothetical |
| Sauron p438 | NY12 p436 | 1E-92 | (p)ppGpp Synthetase |
| Sauron p439 | NY12 p437 | 5E-114 | Hypothetical |
| Sauron p440 | NY12 p438 | 2E-56 | Hypothetical |
| Sauron p441 | NY12 p439 | 6E-24 | Hypothetical |
| Sauron p442 | NY12 p440 | 8E-50 | Hypothetical |
| Sauron p443 | NY12 p441 | 1E-75 | Hypothetical |
| Sauron p444 | NY12 p442 | 3E-93 | Hypothetical |
| Sauron p445 | NY12 p443 | 7E-38 | Hypothetical |
| Sauron p446 | NY12 p444 | 3E-99 | Hypothetical |

Table 3: NY12 Evidence Table

| Gene | Putative Function | Evidence | | | | |
|---|---|---|---|---|---|---|
| | | Blastp | | | Interpro | TMHMM/Signal P |
| | | Description | Source | E-value | | |
| NY12 p001 | Hypothetical | | | | | |
| NY12 p002 | Hypothetical | | | | | |
| NY12 p003 | Hypothetical | | | | | |
| NY12 p004 | Hypothetical | | | | | |
| NY12 p005 | Hypothetical | | | | | |
| NY12 p006 | Hypothetical | | | | | |
| NY12 p007 | Hypothetical | | | | | |
| NY12 p008 | Hypothetical | | | | | |
| NY12 p009 | Hypothetical | | | | | |
| NY12 p010 | Hypothetical | | | | | |
| NY12 p011 | Hypothetical | | | | | |
| NY12 p012 | Hypothetical | | | | | |
| NY12 p013 | Hypothetical | | | | | |
| NY12 p014 | Hypothetical | | | | | |
| NY12 p015 | Hypothetical | | | | | |
| NY12 p016 | Hypothetical | | | | | |
| NY12 p017 | Hypothetical | | | | | |
| NY12 p018 | Hypothetical | | | | | |
| NY12 p019 | Hypothetical | | | | | |
| NY12 p020 | Hypothetical | | | | | |
| NY12 p021 | Hypothetical | | | | | |
| NY12 p022 | Hypothetical | | | | | |
| NY12 p023 | Hypothetical | | | | | |
| NY12 p024 | Hypothetical | | | | | |

| Gene | Putative Function | Evidence | | | | |
|---|---|---|---|---|---|---|
| | | Blastp | | | Interpro | TMHMM/Signal P |
| | | Description | Source | E-value | | |
| NY12 p025 | Hypothetical | | | | | |
| NY12 p026 | Hypothetical | | | | | |
| NY12 p027 | Hypothetical | | | | | |
| NY12 p028 | Hypothetical | | | | | |
| NY12 p029 | Hypothetical | | | | | |
| NY12 p030 | Hypothetical | | | | | |
| NY12 p031 | Hypothetical | | | | | |
| NY12 p032 | Hypothetical | | | | | |
| NY12 p033 | Hypothetical | | | | | |
| NY12 p034 | Hypothetical | | | | | |
| NY12 p035 | Hypothetical | | | | | |
| NY12 p036 | Hypothetical | | | | | |
| NY12 p037 | Hypothetical | | | | | |
| NY12 p038 | Hypothetical | | | | | |
| NY12 p039 | Hypothetical | | | | | |
| NY12 p040 | Hypothetical | | | | | |
| NY12 p041 | Hypothetical | | | | | |
| NY12 p042 | Hypothetical | | | | | |
| NY12 p043 | Hypothetical | | | | | |
| NY12 p044 | Hypothetical | | | | | |
| NY12 p045 | Hypothetical | | | | | |
| NY12 p046 | Hypothetical | | | | | |
| NY12 p047 | Hypothetical | | | | | |
| NY12 p048 | Hypothetical | | | | | |
| NY12 p049 | Hypothetical | | | | | |
| NY12 p050 | Hypothetical | | | | | |
| NY12 p051 | Hypothetical | | | | | |

| Gene | Putative Function | Evidence | | | | |
|---|---|---|---|---|---|---|
| | | Blastp | | | Interpro | TMHMM/Signal P |
| | | Description | Source | E-value | | |
| NY12 p052 | Hypothetical | | | | | |
| NY12 p053 | Hypothetical | | | | | |
| NY12 p054 | Hypothetical | | | | | |
| NY12 p055 | Hypothetical | | | | | |
| NY12 p056 | Hypothetical | | | | | |
| NY12 p057 | Hypothetical | | | | | |
| NY12 p058 | Hypothetical | | | | | |
| NY12 p059 | Hypothetical | | | | | |
| NY12 p060 | Hypothetical | | | | | |
| NY12 p061 | Hypothetical | | | | | |
| NY12 p062 | Hypothetical | | | | | |
| NY12 p063 | Hypothetical | | | | | |
| NY12 p064 | Hypothetical | | | | | |
| NY12 p065 | Hypothetical | | | | | |
| NY12 p066 | Hypothetical | | | | | |
| NY12 p067 | Hypothetical | | | | | |
| NY12 p068 | Hypothetical | | | | | |
| NY12 p069 | Hypothetical | | | | | |
| NY12 p070 | Homing Endonuclease (GIY-YIG) | putative homing endonuclease GIY-YIG family | Aeromonas phageAes508 | 1.46908E-08 | IPR000305, IPR006350, IPR009057, IPR027299 | |
| NY12 p071 | Hypothetical | | | | | |
| NY12 p072 | Hypothetical | | | | | |
| NY12 p073 | Hypothetical | | | | | |
| NY12 p074 | Hypothetical | | | | | |
| NY12 p075 | Hypothetical | | | | | |
| NY12 p076 | Tail Tube Protein | gp19 tail tube protein | Enterobacteria phageT4 | 3.18043E-12 | | |
| NY12 p077 | Hypothetical | | | | | |
| NY12 p078 | Tail Sheath Protein | gp18 tail sheath protein | Enterobacteria phageT4 | 2.50274E-27 | IPR007067 | |

| Gene | Putative Function | Evidence | | | | |
|---|---|---|---|---|---|---|
| | | Blastp | | | Interpro | TMHMM/Signal P |
| | | Description | Source | E-value | | |
| NY12 p079 | Hypothetical | | | | | |
| NY12 p080 | Hypothetical | | | | | |
| NY12 p081 | Hypothetical | | | | | |
| NY12 p082 | Hypothetical | | | | | |
| NY12 p083 | Hypothetical | | | | | |
| NY12 p084 | Hypothetical | | | | | |
| NY12 p085 | Hypothetical | | | | | |
| NY12 p086 | Hypothetical | | | | | |
| NY12 p087 | Hypothetical | | | | | |
| NY12 p088 | SNF2-like Helicase | SNF2-related protein | Thermoanaerobacterium phageTHSA-485A | 2.2202E-09 | IPR000330 | |
| NY12 p089 | Hypothetical | | | | | |
| NY12 p090 | Hypothetical | | | | | |
| NY12 p091 | HNH Endonuclease | HNH endonuclease | Ralstonia phageRSL1 | 4.0657E-40 | IPR002711, IPR003615 | |
| NY12 p092 | Hypothetical | | | | | |
| NY12 p093 | Hypothetical | | | | | |
| NY12 p094 | Hypothetical | | | | | |
| NY12 p095 | Hypothetical | | | | | |
| NY12 p096 | Hypothetical | | | | | |
| NY12 p097 | Hypothetical | | | | | |
| NY12 p098 | Cytidine/Deoxycytidine Deaminase | cytidine and deoxycytidylate deaminase zinc-binding region | Pseudomonas phagephi_Pto-bp6g | 5.2468E-21 | IPR002125, IPR015517, IPR016193 | |
| NY12 p099 | Hypothetical | | | | | |
| NY12 p100 | NUDIX Hydrolase Domain | MutT/NUDIX hydrolase family protein | Ralstonia phageRSL1 | 4.76419E-24 | IPR000086, IPR015797, IPR020084 | |
| NY12 p101 | Hypothetical | | | | | |
| NY12 p102 | Hypothetical | | | | | |
| NY12 p103 | Hypothetical | | | | | |
| NY12 p104 | Hypothetical | | | | | |
| NY12 p105 | Hypothetical | | | | | |

| Gene | Putative Function | Evidence | | | | |
|---|---|---|---|---|---|---|
| | | Blastp | | | Interpro | TMHMM/Signal P |
| | | Description | Source | E-value | | |
| NY12 p106 | Hypothetical | | | | | |
| NY12 p107 | Hypothetical | | | | | |
| NY12 p108 | Hypothetical | | | | | |
| NY12 p109 | Hypothetical | | | | | |
| NY12 p110 | Kelch-motif Containing Protein | kelch motif-containing protein | Corallococcus coralloides DSM 2259 | 6.62E-05 | IPR015916 | |
| NY12 p111 | Hypothetical | | | | | |
| NY12 p112 | Hypothetical | | | | | |
| NY12 p113 | Nicotinate Phosphoribosyltransferase | nicotinate phosphoribosyltransferase | Ralstonia phageRSL1 | 0 | IPR015977, IPR016471 | |
| NY12 p114 | Hypothetical | | | | | |
| NY12 p115 | Putative Cytidyltransferase | | | | IPR004821, IPR015797 | |
| NY12 p116 | Hypothetical | | | | | |
| NY12 p117 | NAD-dependent DNA Ligase | NAD-dependent DNA ligase | Ralstonia phageRSL1 | 0 | IPR004150, IPR012340, IPR013839, IPR013840 | |
| NY12 p118 | Hypothetical | | | | | |
| NY12 p119 | Acyl Carrier Protein-like | | | | IPR009081 | |
| NY12 p120 | Hypothetical | | | | | |
| NY12 p121 | Hypothetical | | | | | |
| NY12 p122 | Hypothetical | | | | | |
| NY12 p123 | Hypothetical | | | | | |
| NY12 p124 | Hypothetical | | | | | |
| NY12 p125 | Hypothetical | | | | | |
| NY12 p126 | Hypothetical | | | | | |
| NY12 p127 | Putative Phosphatase | | | | IPR029052 | |
| NY12 p128 | HNH Endonuclease | putative HNH endonuclease | Deftia phagephiW-14 | 1.61628E-14 | IPR002711 | |
| NY12 p129 | Hypothetical | | | | | |
| NY12 p130 | Aspartyl/glutamyl-tRNA Amidotransferase Subunit B-like | | | | IPR003789, IPR023168 | |
| NY12 p131 | RtcB-like Protein | putative RtcB-like protein | Caulobacter phageCcrColossus | 3.6743E-139 | IPR001233 | |
| NY12 p132 | NUDIX Hydrolase | NudE nudix hydrolase | Enterobacteria phageRB43 | 5.24172E-06 | IPR000086, IPR015797, IPR020084, IPR020476 | |

| Gene | Putative Function | Evidence | | | | |
|---|---|---|---|---|---|---|
| | | Blastp | | | Interpro | TMHMM/Signal P |
| | | Description | Source | E-value | | |
| NY12 p133 | Hypothetical | | | | | |
| NY12 p134 | Hypothetical | | | | | |
| NY12 p135 | Hypothetical | | | | | |
| NY12 p136 | Hypothetical | | | | | |
| NY12 p137 | Hypothetical | | | | | |
| NY12 p138 | Hypothetical | | | | | |
| NY12 p139 | Hypothetical | | | | | |
| NY12 p140 | Hypothetical | | | | | |
| NY12 p141 | Hypothetical | | | | | |
| NY12 p142 | Hypothetical | | | | | |
| NY12 p143 | Hypothetical | | | | | |
| NY12 p144 | Hypothetical | | | | | |
| NY12 p145 | Hypothetical | | | | | |
| NY12 p146 | Hypothetical | | | | | |
| NY12 p147 | Hypothetical | | | | | |
| NY12 p148 | Hypothetical | | | | | |
| NY12 p149 | Hypothetical | | | | | |
| NY12 p150 | Hypothetical | | | | | |
| NY12 p151 | Hypothetical | | | | | |
| NY12 p152 | Hypothetical | | | | | |
| NY12 p153 | Hypothetical | | | | | |
| NY12 p154 | Hypothetical | | | | | |
| NY12 p155 | Hypothetical | | | | | |
| NY12 p156 | Hypothetical | | | | | |
| NY12 p157 | Hypothetical | | | | | |
| NY12 p158 | Hypothetical | | | | | |
| NY12 p159 | Hypothetical | | | | | |

| Gene | Putative Function | Evidence | | | | |
|---|---|---|---|---|---|---|
| | | Blastp | | | Interpro | TMHMM/Signal P |
| | | Description | Source | E-value | | |
| NY12 p160 | Putative RNA Ligase | putative RNA ligase, DRB0094 family | Aeromonas phageAes508 | 1.64E-68 | IPR012646, IPR021122 | |
| NY12 p161 | Hypothetical | | | | | |
| NY12 p162 | Hypothetical | | | | | |
| NY12 p163 | Hypothetical | | | | | |
| NY12 p164 | Putative Homing Endonuclease | putativel Seg-like homing endonuclease, GIY-YIG family | Cronobacter phagevB_CsaM_GAP161 | 9.11485E-05 | IPR003611 | |
| NY12 p165 | Hypothetical | | | | | |
| NY12 p166 | Hypothetical | | | | | |
| NY12 p167 | Hypothetical | | | | | |
| NY12 p168 | Hypothetical | | | | | |
| NY12 p169 | Type IIA DNA Topoisomerase, GyrA-like | type IIA topoisomerase | Ralstonia phageRSL1 | 0 | IPR002205, IPR013758, IPR013760 | |
| NY12 p170 | Type IIA DNA Topoisomerase, GyrB-like | type IIA topoisomerase | Ralstonia phageRSL1 | 0 | IPR001241, IPR002288, IPR003594, IPR013506, IPR013760 | |
| NY12 p171 | Hypothetical | | | | | |
| NY12 p172 | Hypothetical | | | | | |
| NY12 p173 | Hypothetical | | | | | |
| NY12 p174 | Hypothetical | | | | | |
| NY12 p175 | Hypothetical | | | | | |
| NY12 p176 | Hypothetical | | | | | |
| NY12 p177 | Hypothetical | | | | | |
| NY12 p178 | Hypothetical | | | | | |
| NY12 p179 | Hypothetical | | | | | |
| NY12 p180 | Hypothetical | | | | | |
| NY12 p181 | Hypothetical | | | | | |
| NY12 p182 | Hypothetical | | | | | |
| NY12 p183 | Hypothetical | | | | | |
| NY12 p184 | Hypothetical | | | | | |
| NY12 p185 | Hypothetical | | | | | |
| NY12 p186 | Hypothetical | | | | | |

| Gene | Putative Function | Evidence | | | | |
|---|---|---|---|---|---|---|
| | | Blastp | | | Interpro | TMHMM/Signal P |
| | | Description | Source | E-value | | |
| NY12 p187 | Hypothetical | | | | | |
| NY12 p188 | Hypothetical | | | | | |
| NY12 p189 | Hypothetical | | | | | |
| NY12 p190 | Hypothetical | | | | | |
| NY12 p191 | Hypothetical | | | | | |
| NY12 p192 | Recombination Endonuclease-like Protein | gp47 recombination endonuclease subunit | Enterobacteria phageT4 | 1.08122E-11 | IPR024654 | |
| NY12 p193 | Hypothetical | | | | | |
| NY12 p194 | DEAD Type Helicase | | | | IPR011545 | |
| NY12 p195 | Hypothetical | | | | | |
| NY12 p196 | Hypothetical | | | | | |
| NY12 p197 | Hypothetical | | | | | |
| NY12 p198 | Hypothetical | | | | | |
| NY12 p199 | Hypothetical | | | | | |
| NY12 p200 | Hypothetical | | | | | |
| NY12 p201 | Hypothetical | | | | | |
| NY12 p202 | Hypothetical | | | | | |
| NY12 p203 | Hypothetical | | | | | |
| NY12 p204 | Hypothetical | | | | | |
| NY12 p205 | Hypothetical | | | | | |
| NY12 p206 | Hypothetical | | | | | |
| NY12 p207 | Hypothetical | | | | | |
| NY12 p208 | Hypothetical | | | | | |
| NY12 p209 | Hypothetical | | | | | |
| NY12 p210 | Hypothetical | | | | | |
| NY12 p211 | GroES-like Protein | GroES | Bacillus phage0305phi8-36 | 2.33734E-07 | IPR011032, IPR018369, IPR020818 | |
| NY12 p212 | Thioredoxin | hypothetical host-like thioredoxin | Roseovarius Plymouth podovirus1 | 1.18542E-12 | IPR005746, IPR012336, IPR013766, IPR017937 | |
| NY12 p213 | Hypothetical | | | | | |

| Gene | Putative Function | Evidence | | | | |
|---|---|---|---|---|---|---|
| | | Blastp | | | Interpro | TMHMM/Signal P |
| | | Description | Source | E-value | | |
| NY12 p214 | Hypothetical | | | | | |
| NY12 p215 | Hypothetical | | | | | |
| NY12 p216 | RecD-like Protein | RecD like protein | Ralstonia phageRSL1 | 2.0053E-114 | | |
| NY12 p217 | Endodeoxyribonuclease | endodeoxyribonuclease | Escherichia coliSTEC_94C | 5.05722E-11 | | |
| NY12 p218 | Hypothetical | | | | | |
| NY12 p219 | Hypothetical | | | | | |
| NY12 p220 | Hypothetical | | | | | |
| NY12 p221 | Metal Dependent Phosphohydrolase-like Protein | metal dependent phosphohydrolases like protein | Ralstonia phageRSL1 | 1.53083E-15 | | |
| NY12 p222 | DNA Polymerase I | DNA polymerase I | Ralstonia phageRSL1 | 0 | IPR001098, IPR002298, IPR002562, IPR012337 | |
| NY12 p223 | Hypothetical | | | | | |
| NY12 p224 | Hypothetical | | | | | |
| NY12 p225 | DNA Primase | DNA primase | Ralstonia phageRSL1 | 2.024E-93 | | |
| NY12 p226 | Putative i-spanin | | | | TM:1 7-29 N:in C:out SPII: 29-30 | |
| NY12 p227 | Putative o-spanin | | | | SPII: 19-20, G | |
| NY12 p228 | Hypothetical | | | | | |
| NY12 p229 | Homing Endonuclease | | | | IPR003611 | |
| NY12 p230 | Hypothetical | | | | | |
| NY12 p231 | Hypothetical | | | | | |
| NY12 p232 | Hypothetical | | | | | |
| NY12 p233 | Hypothetical | | | | | |
| NY12 p234 | Hypothetical | | | | | |
| NY12 p235 | Hypothetical | | | | | |
| NY12 p236 | GIY-YIG Endonuclease | putative GIY-YIG endonuclease | Serratia phagephiMAM1 | 2.91639E-08 | IPR000305, IPR027299, | |
| NY12 p237 | Thymidylate Synthase | thymidilate synthase | Escherichia phagevB_EcoP_G7C | 1.25E-56 | IPR003669 | |
| NY12 p238 | Hypothetical | | | | | |
| NY12 p239 | Hypothetical | | | | | |
| NY12 p240 | Hypothetical | | | | | |

| Gene | Putative Function | Evidence | | | | |
|---|---|---|---|---|---|---|
| | | Blastp | | | Interpro | TMHMM/Signal P |
| | | Description | Source | E-value | | |
| NY12 p241 | Hypothetical | | | | | |
| NY12 p242 | RecA-like Recombinase | Rec A-like recombinase | Ralstonia phageRSL1 | 1.0851E-176 | | |
| NY12 p243 | Hypothetical | | | | | |
| NY12 p244 | Terminase | | | | | xxx |
| NY12 p245 | RuvC Resolvase-like Protein | RuvC_resolvase like protein | Ralstonia phageRSL1 | 1.60218E-53 | | |
| NY12 p246 | Hypothetical | | | | | |
| NY12 p247 | Hypothetical | | | | | |
| NY12 p248 | Hypothetical | | | | | |
| NY12 p249 | Hypothetical | | | | | |
| NY12 p250 | Hypothetical | | | | | |
| NY12 p251 | Hypothetical | | | | | |
| NY12 p252 | Hypothetical | | | | | |
| NY12 p253 | Hypothetical | | | | | |
| NY12 p254 | Hypothetical | | | | | |
| NY12 p255 | Hypothetical | | | | | |
| NY12 p256 | Tail Protein | phage tail protein | CyanophagePSS2 | 5.19716E-11 | IPR023346 | |
| NY12 p257 | Hypothetical | | | | | |
| NY12 p258 | Hypothetical | | | | | |
| NY12 p259 | Hypothetical | | | | | |
| NY12 p260 | Hypothetical | | | | | |
| NY12 p261 | Baseplate Wedge Subunit | gp25 baseplate wedge subunit | Enterobacteria phageT4 | 2.87913E-06 | | |
| NY12 p262 | Structural Protein | putative base plate wedget subunit protein | Pseudomonas phageLu11 | 2.29239E-17 | | |
| NY12 p263 | Hypothetical | | | | | |
| NY12 p264 | Phage Tail Collar Protein | phage tail collar domain protein | Ralstonia phageRSL1 | 5.02011E-86 | IPR022225 | |
| NY12 p265 | Hypothetical | | | | | |
| NY12 p266 | Hypothetical | | | | | |
| NY12 p267 | Hypothetical | | | | | |

| Gene | Putative Function | Evidence | | | | |
|---|---|---|---|---|---|---|
| | | Blastp | | | Interpro | TMHMM/Signal P |
| | | Description | Source | E-value | | |
| NY12 p268 | Hypothetical | | | | | |
| NY12 p269 | Hypothetical | | | | | |
| NY12 p270 | Hypothetical | | | | | |
| NY12 p271 | Hypothetical | | | | | |
| NY12 p272 | Putative Tail Fiber Protein | Burkholderia phageBcepNazgul | 1.6183E-09 | IPR008979 | | |
| NY12 p273 | Hypothetical | | | | | |
| NY12 p274 | Hypothetical | | | | | |
| NY12 p275 | Hypothetical | | | | | |
| NY12 p276 | Hypothetical | | | | | |
| NY12 p277 | Hypothetical | | | | | |
| NY12 p278 | Hypothetical | | | | | |
| NY12 p279 | Hypothetical | | | | | |
| NY12 p280 | Putative Long Tail Fiber Protein | gp37 long tail fiber distal subunit | Enterobacteria phageJS98 | 2.11397E-08 | | |
| NY12 p281 | Hypothetical | | | | | |
| NY12 p282 | Putative Endolysin (GH19) | putative lyzozyme | Pseudomonas phageSN | 8.04706E-32 | IPR000726, IPR023346 | |
| NY12 p283 | Putative Antiholin | | | | | TM:1 22-44 N:out C:in |
| NY12 p284 | Putative Type 1 Holin | phage holin | Psychrobacter phagePsymv2 | 1.56E-15 | | TM:3 10-29, 41-60, 70-92 N:out C:in |
| NY12 p285 | Hypothetical | | | | | |
| NY12 p286 | 5'-3' Exonuclease | 5'-3' exonuclease | Ralstonia phageRSL1 | 1.70171E-67 | IPR002421, IPR020045, IPR020046 | |
| NY12 p287 | Putative Structural Protein | phage tail collar domain protein | Ralstonia phageRSL1 | 4.7371E-10 | IPR022225 | |
| NY12 p288 | Hypothetical | | | | | |
| NY12 p289 | Hypothetical | | | | | |
| NY12 p290 | Hypothetical | | | | | |
| NY12 p291 | Hypothetical | | | | | |
| NY12 p292 | Hypothetical | | | | | |
| NY12 p293 | Hypothetical | | | | | |
| NY12 p294 | Hypothetical | | | | | |

| Gene | Putative Function | Evidence | | | | |
|---|---|---|---|---|---|---|
| | | Blastp | | | Interpro | TMHMM/Signal P |
| | | Description | Source | E-value | | |
| NY12 p295 | DNA Polymerase III-like Protein | DNA polymerase III gamma/tau subunit-like protein | Ralstonia phageRSL1 | 8.1376E-143 | IPR003593 | |
| NY12 p296 | ATPase Domain Containing Protein | putative ATPase involved in DNA repair | Pseudomonas phageLu11 | 9.13486E-29 | | |
| NY12 p297 | Hypothetical | | | | | |
| NY12 p298 | Hypothetical | | | | | |
| NY12 p299 | Hypothetical | | | | | |
| NY12 p300 | Hypothetical | | | | | |
| NY12 p301 | DNA Polymerase III Beta Subunit-like | beta clamp domain-like protein | Ralstonia phageRSL1 | 3.2545E-101 | | |
| NY12 p302 | Hypothetical | | | | | |
| NY12 p303 | Hypothetical | | | | | |
| NY12 p304 | Hypothetical | | | | | |
| NY12 p305 | Hypothetical | | | | | |
| NY12 p306 | Hypothetical | | | | | |
| NY12 p307 | Hypothetical | | | | | |
| NY12 p308 | ATP-Dependent Helicase | putative DNA/RNA helicase | Pseudomonas phageLu11 | 7.88319E-67 | IPR001650, IPR006935, IPR014001 | |
| NY12 p309 | Hypothetical | | | | | |
| NY12 p310 | Hypothetical | | | | | |
| NY12 p311 | Hypothetical | | | | | |
| NY12 p312 | Hypothetical | | | | | |
| NY12 p313 | Hypothetical | | | | | |
| NY12 p314 | Hypothetical | | | | | |
| NY12 p315 | Hypothetical | | | | | |
| NY12 p316 | Replicative DNA Helicase | replicative DNA helicase | Ralstonia phageRSL1 | 8.8092E-156 | IPR007694 | |
| NY12 p317 | Hypothetical | | | | | |
| NY12 p318 | Hypothetical | | | | | |
| NY12 p319 | Hypothetical | | | | | |
| NY12 p320 | Hypothetical | | | | | |
| NY12 p321 | Hypothetical | | | | | |

| Gene | Putative Function | Evidence | | | | |
|---|---|---|---|---|---|---|
| | | Blastp | | | Interpro | TMHMM/Signal P |
| | | Description | Source | E-value | | |
| NY12 p322 | Hypothetical | | | | | |
| NY12 p323 | Hypothetical | | | | | |
| NY12 p324 | Hypothetical | | | | | |
| NY12 p325 | Hypothetical | | | | | |
| NY12 p326 | Hypothetical | | | | | |
| NY12 p327 | Hypothetical | | | | | |
| NY12 p328 | Hypothetical | | | | | |
| NY12 p329 | Hypothetical | | | | | |
| NY12 p330 | Hypothetical | | | | | |
| NY12 p331 | Hypothetical | | | | | |
| NY12 p332 | tRNA His Guanylyltransferase Thg1 | putative Thg1 | Pseudomonas phage201phi2-1 | 2.16131E-53 | IPR007537, IPR024956, IPR025845 | |
| NY12 p333 | Hypothetical | | | | | |
| NY12 p334 | Hypothetical | | | | | |
| NY12 p335 | Hypothetical | | | | | |
| NY12 p336 | Hypothetical | | | | | |
| NY12 p337 | Hypothetical | | | | | |
| NY12 p338 | Hypothetical | | | | | |
| NY12 p339 | Hypothetical | | | | | |
| NY12 p340 | Hypothetical | | | | | |
| NY12 p341 | Hypothetical | | | | | |
| NY12 p342 | Hypothetical | | | | | |
| NY12 p343 | Hypothetical | | | | | |
| NY12 p344 | Hypothetical | | | | | |
| NY12 p345 | Hypothetical | | | | | |
| NY12 p346 | Hypothetical | | | | | |
| NY12 p347 | Hypothetical | | | | | |
| NY12 p348 | Hypothetical | | | | | |

| Gene | Putative Function | Evidence | | | | |
|---|---|---|---|---|---|---|
| | | Blastp | | | Interpro | TMHMM/Signal P |
| | | Description | Source | E-value | | |
| NY12 p349 | Hypothetical | | | | | |
| NY12 p350 | Hypothetical | | | | | |
| NY12 p351 | Hypothetical | | | | | |
| NY12 p352 | Hypothetical | | | | | |
| NY12 p353 | Hypothetical | | | | | |
| NY12 p354 | Hypothetical | | | | | |
| NY12 p355 | Hypothetical | | | | | |
| NY12 p356 | Hypothetical | | | | | |
| NY12 p357 | Hypothetical | | | | | |
| NY12 p358 | Hypothetical | | | | | |
| NY12 p359 | Hypothetical | | | | | |
| NY12 p360 | Hypothetical | | | | | |
| NY12 p361 | Hypothetical | | | | | |
| NY12 p362 | Hypothetical | | | | | |
| NY12 p363 | Hypothetical | | | | | |
| NY12 p364 | Hypothetical | | | | | |
| NY12 p365 | Hypothetical | | | | | |
| NY12 p366 | Hypothetical | | | | | |
| NY12 p367 | Hypothetical | | | | | |
| NY12 p368 | Hypothetical | | | | | |
| NY12 p369 | Hypothetical | | | | | |
| NY12 p370 | T4 RnlA-like RNA ligase and Tail Fiber Attachment Catalyst | RnlA RNA ligase 1 and tail fiber attachment catalyst | Enterobacteria phageT4 | 4.22184E-22 | IPR019039 | |
| NY12 p371 | Hypothetical | | | | | |
| NY12 p372 | Hypothetical | | | | | |
| NY12 p373 | Hypothetical | | | | | |
| NY12 p374 | Putative Nucleotidyltransferase | putative nucleotidyltransferase protein | Caulobacter phageCcrColossus | 1.60256E-29 | IPR018775 | |
| NY12 p375 | Hypothetical | | | | | |

| Gene | Putative Function | Evidence | | | | |
|---|---|---|---|---|---|---|
| | | Blastp | | | Interpro | TMHMM/Signal P |
| | | Description | Source | E-value | | |
| NY12 p376 | Hypothetical | | | | | |
| NY12 p377 | Hypothetical | | | | | |
| NY12 p378 | Hypothetical | | | | | |
| NY12 p379 | Hypothetical | | | | | |
| NY12 p380 | Hypothetical | | | | | |
| NY12 p381 | Hypothetical | | | | | |
| NY12 p382 | Hypothetical | | | | | |
| NY12 p383 | Hypothetical | | | | | |
| NY12 p384 | Hypothetical | | | | | |
| NY12 p385 | Hypothetical | | | | | |
| NY12 p386 | Hypothetical | | | | | |
| NY12 p387 | Hypothetical | | | | | |
| NY12 p388 | Hypothetical | | | | | |
| NY12 p389 | Hypothetical | | | | | |
| NY12 p390 | Hypothetical | | | | | |
| NY12 p391 | Hypothetical | | | | | |
| NY12 p392 | Hypothetical | | | | | |
| NY12 p393 | Hypothetical | | | | | |
| NY12 p394 | Hypothetical | | | | | |
| NY12 p395 | Hypothetical | | | | | |
| NY12 p396 | Hypothetical | | | | | |
| NY12 p397 | Hypothetical | | | | | |
| NY12 p398 | Hypothetical | | | | | |
| NY12 p399 | Hypothetical | | | | | |
| NY12 p400 | Hypothetical | | | | | |
| NY12 p401 | Hypothetical | | | | | |
| NY12 p402 | Hypothetical | | | | | |

| Gene | Putative Function | Evidence | | | | |
|---|---|---|---|---|---|---|
| | | Blastp | | | Interpro | TMHMM/Signal P |
| | | Description | Source | E-value | | |
| NY12 p403 | Hypothetical | | | | | |
| NY12 p404 | Hypothetical | | | | | |
| NY12 p405 | Hypothetical | | | | | |
| NY12 p406 | Hypothetical | | | | | |
| NY12 p407 | Hypothetical | | | | | |
| NY12 p408 | Hypothetical | | | | | |
| NY12 p409 | Hypothetical | | | | | |
| NY12 p410 | Hypothetical | | | | | |
| NY12 p411 | Bacteriophage-Associated Superinfection Exclusion Protein | putative imm immunity to superinfection membrane protein | Salmonella phagevB_SenS-Ent1 | 2.791E-07 | IPR016410 | TM:2 15-34, 41-63 N:out C:out |
| NY12 p412 | Bacteriophage-Associated Superinfection Exclusion Protein | putative membrane immunity protein | Escherichia phagevB_EcoP_G7C | 9.40907E-10 | IPR016410 | TM:2 2-24, 34-56 N:in C:in |
| NY12 p413 | Hypothetical | | | | | |
| NY12 p414 | Hypothetical | | | | | |
| NY12 p415 | Hypothetical | | | | | |
| NY12 p416 | Hypothetical | | | | | |
| NY12 p417 | Hypothetical | | | | | |
| NY12 p418 | Hypothetical | | | | | |
| NY12 p419 | Hypothetical | | | | | |
| NY12 p420 | Hypothetical | | | | | |
| NY12 p421 | Hypothetical | | | | | |
| NY12 p422 | Hypothetical | | | | | |
| NY12 p423 | Hypothetical | | | | | |
| NY12 p424 | Hypothetical | | | | | |
| NY12 p425 | Hypothetical | | | | | |
| NY12 p426 | Hypothetical | | | | | |
| NY12 p427 | Hypothetical | | | | | |
| NY12 p428 | Hypothetical | | | | | |
| NY12 p429 | Hypothetical | | | | | |

| Gene | Putative Function | Evidence | | | | |
|---|---|---|---|---|---|---|
| | | Blastp | | | Interpro | TMHMM/Signal P |
| | | Description | Source | E-value | | |
| NY12 p430 | Hypothetical | | | | | |
| NY12 p431 | Hypothetical | | | | | |
| NY12 p432 | Hypothetical | | | | | |
| NY12 p433 | Hypothetical | | | | | |
| NY12 p434 | Hypothetical | | | | | |
| NY12 p435 | Hypothetical | | | | | |
| NY12 p436 | (p)ppGpp Synthetase | Guanosine-3',5'-bis(Diphosphate) 3'-pyrophosphohydrolase | Streptococcus pneumoniaeSPNA45 | 4.36211E-08 | IPR026020 | |
| NY12 p437 | Hypothetical | | | | | |
| NY12 p438 | Hypothetical | | | | | |
| NY12 p439 | Hypothetical | | | | | |
| NY12 p440 | Hypothetical | | | | | |
| NY12 p441 | Hypothetical | | | | | |
| NY12 p442 | Hypothetical | | | | | |
| NY12 p443 | Hypothetical | | | | | |
| NY12 p444 | Hypothetical | | | | | |
| NY12 p445 | Hypothetical | | | | | |

Table 4: Sauron Evidence Table

| Gene | Putative Function | Evidence | | | | |
|---|---|---|---|---|---|---|
| | | Blastp | | | Interpro | TMHMM/Signal P |
| | | Description | Source | E-value | | |
| Sauron p001 | Hypothetical | | | | | |
| Sauron p002 | Hypothetical | | | | | |
| Sauron p003 | Hypothetical | | | | | |
| Sauron p004 | Hypothetical | | | | | |
| Sauron p005 | Hypothetical | | | | | |
| Sauron p006 | Hypothetical | | | | | |
| Sauron p007 | Hypothetical | | | | | |
| Sauron p008 | Hypothetical | | | | | |
| Sauron p009 | Hypothetical | | | | | |
| Sauron p010 | Hypothetical | | | | | |
| Sauron p011 | Hypothetical | | | | | |
| Sauron p012 | Hypothetical | | | | | |
| Sauron p013 | Hypothetical | | | | | |
| Sauron p014 | Hypothetical | | | | | |
| Sauron p015 | Hypothetical | | | | | |
| Sauron p016 | Hypothetical | | | | | |
| Sauron p017 | Hypothetical | | | | | |
| Sauron p018 | Hypothetical | | | | | |
| Sauron p019 | Hypothetical | | | | | |
| Sauron p020 | Hypothetical | | | | | |
| Sauron p021 | Hypothetical | | | | | |
| Sauron p022 | Hypothetical | | | | | |
| Sauron p023 | Hypothetical | | | | | |
| Sauron p024 | Hypothetical | | | | | |
| Sauron p025 | Hypothetical | | | | | |
| Sauron p026 | Hypothetical | | | | | |

| Gene | Putative Function | Evidence | | | | |
|---|---|---|---|---|---|---|
| | | Blastp | | | Interpro | TMHMM/Signal P |
| | | Description | Source | E-value | | |
| Sauron p027 | Hypothetical | | | | | |
| Sauron p028 | Hypothetical | | | | | |
| Sauron p029 | Hypothetical | | | | | |
| Sauron p030 | Hypothetical | | | | | |
| Sauron p031 | Hypothetical | | | | | |
| Sauron p032 | Hypothetical | | | | | |
| Sauron p033 | Hypothetical | | | | | |
| Sauron p034 | Hypothetical | | | | | |
| Sauron p035 | Hypothetical | | | | | |
| Sauron p036 | Hypothetical | | | | | |
| Sauron p037 | Hypothetical | | | | | |
| Sauron p038 | Hypothetical | | | | | |
| Sauron p039 | Hypothetical | | | | | |
| Sauron p040 | Hypothetical | | | | | |
| Sauron p041 | Hypothetical | | | | | |
| Sauron p042 | Hypothetical | | | | | |
| Sauron p043 | Hypothetical | | | | | |
| Sauron p044 | Hypothetical | | | | | |
| Sauron p045 | Hypothetical | | | | | |
| Sauron p046 | Hypothetical | | | | | |
| Sauron p047 | Hypothetical | | | | | |
| Sauron p048 | Hypothetical | | | | | |
| Sauron p049 | Hypothetical | | | | | |
| Sauron p050 | Hypothetical | | | | | |
| Sauron p051 | Hypothetical | | | | | |
| Sauron p052 | Hypothetical | | | | | |
| Sauron p053 | Hypothetical | | | | | |
| Sauron p054 | Hypothetical | | | | | |

| Gene | Putative Function | Evidence | | | | |
|---|---|---|---|---|---|---|
| | | Blastp | | | Interpro | TMHMM/Signal P |
| | | Description | Source | E-value | | |
| Sauron p055 | Hypothetical | | | | | |
| Sauron p056 | Hypothetical | | | | | |
| Sauron p057 | Hypothetical | | | | | |
| Sauron p058 | Hypothetical | | | | | |
| Sauron p059 | Hypothetical | | | | | |
| Sauron p060 | Hypothetical | | | | | |
| Sauron p061 | Hypothetical | | | | | |
| Sauron p062 | Hypothetical | | | | | |
| Sauron p063 | Hypothetical | | | | | |
| Sauron p064 | Hypothetical | | | | | |
| Sauron p065 | Hypothetical | | | | | |
| Sauron p066 | Hypothetical | | | | | |
| Sauron p067 | Hypothetical | | | | | |
| Sauron p068 | Hypothetical | | | | | |
| Sauron p069 | Hypothetical | | | | | |
| Sauron p070 | Homing Endonuclease (GIY-YIG) | GIY-YIG endonuclease | Ceratocystis cacaofunesta | 5E-10 | IPR000305, IPR027299 | |
| Sauron p071 | Hypothetical | | | | | |
| Sauron p072 | Hypothetical | | | | | |
| Sauron p073 | Hypothetical | | | | | |
| Sauron p074 | Hypothetical | | | | | |
| Sauron p075 | Hypothetical | | | | | |
| Sauron p076 | Tail Tube Protein | gp19 tail tube protein | Enterobacteria phage T4 | 0.000000003 | | |
| Sauron p077 | Hypothetical | | | | | |
| Sauron p078 | Tail Sheath Protein | tail sheath protein | Enterobacteria phage T4 | 7E-25 | IPR007067 | |
| Sauron p079 | Hypothetical | | | | | |
| Sauron p080 | Hypothetical | | | | | |
| Sauron p081 | Hypothetical | | | | | |
| Sauron p082 | Hypothetical | | | | | |

| Gene | Putative Function | Evidence | | | | |
|---|---|---|---|---|---|---|
| | | Blastp | | | Interpro | TMHMM/Signal P |
| | | Description | Source | E-value | | |
| Sauron p083 | Hypothetical | | | | | |
| Sauron p084 | Hypothetical | | | | | |
| Sauron p085 | Hypothetical | | | | | |
| Sauron p086 | Hypothetical | | | | | |
| Sauron p087 | Hypothetical | | | | | |
| Sauron p088 | SNF2-like Helicase | Multispecies helicase SNF2 | Streptomyces | 0.0000007 | IPR000330, IPR027417 | |
| Sauron p089 | Hypothetical | | | | | |
| Sauron p090 | Hypothetical | | | | | |
| Sauron p091 | Hypothetical | | | | | |
| Sauron p092 | Hypothetical | | | | | |
| Sauron p093 | Hypothetical | | | | | |
| Sauron p094 | Hypothetical | | | | | |
| Sauron p095 | Hypothetical | | | | | |
| Sauron p096 | Hypothetical | | | | | |
| Sauron p097 | Cytidine/Deoxycytidine Deaminase | cytidine deaminase | [Sutterella parvirubra] | 1E-26 | IPR016473, IPR002125, IPR016193 | |
| Sauron p098 | Hypothetical | | | | | |
| Sauron p099 | NUDIX Hydrolase Domain | NUDIX hydrolase | Citrobacter freundii] | 0.000008 | IPR015797, IPR000086, IPR020084 | |
| Sauron p100 | Hypothetical | | | | | |
| Sauron p101 | Hypothetical | | | | | |
| Sauron p102 | Hypothetical | | | | | |
| Sauron p103 | Hypothetical | | | | | |
| Sauron p104 | Hypothetical | | | | | |
| Sauron p105 | Hypothetical | | | | | |
| Sauron p106 | Hypothetical | | | | | |
| Sauron p107 | Hypothetical | | | | | |
| Sauron p108 | Hypothetical | | | | | |
| Sauron p109 | Kelch-motif Containing Protein | kelch motif-containing protein | Corallococcus coralloides | 0.0002 | IPR015916 | |
| Sauron p110 | Hypothetical | | | | | |

| Gene | Putative Function | Evidence | | | | |
|---|---|---|---|---|---|---|
| | | Blastp | | | Interpro | TMHMM/Signal P |
| | | Description | Source | E-value | | |
| Sauron p111 | Hypothetical | | | | | |
| Sauron p112 | Nicotinate Phosphoribosyltransferase | nicotinate phosphoribosyltransferase | Thiothrix flexilis | 5E-162 | IPR016471, IPR007229, IPR002638 | |
| Sauron p113 | Hypothetical | | | | | |
| Sauron p114 | Putative Cytidyltransferase | cytidyltransferase | Variovorax sp. CF313 | 1E-66 | IPR004821, IPR015797, IPR000086 | |
| Sauron p115 | Hypothetical | | | | | |
| Sauron p116 | NAD-dependent DNA Ligase | lig gene product | Ralstonia phage RSL1 | | IPR013840, IPR013839, IPR012340, IPR004150 | |
| Sauron p117 | Hypothetical | | | | | |
| Sauron p118 | Acyl Carrier Protein-like | acyl carrier protein | Clostridium hydrogeniformans | | IPR009081 | |
| Sauron p119 | Hypothetical | | | | | |
| Sauron p120 | Hypothetical | | | | | |
| Sauron p121 | Hypothetical | | | | | |
| Sauron p122 | Hypothetical | | | | | |
| Sauron p123 | Hypothetical | | | | | |
| Sauron p124 | Hypothetical | | | | | |
| Sauron p125 | Hypothetical | | | | | |
| Sauron p126 | Putative Phosphatase | metallophosphatase | Parabacteroides distasonis | 6E-19 | IPR029052 | |
| Sauron p127 | HNH Endonuclease | putative HNH endonuclease | Caulobacter phage CcrColossus | 7E-11 | IPR002711 | |
| Sauron p128 | Hypothetical | | | | | |
| Sauron p129 | Aspartyl/glutamyl-tRNA Amidotransferase Subunit B-like | aspartyl-tRNA amidotransferase subunit B | Desulfovibrio longus | 0.0000001 | IPR003789, IPR023168 | |
| Sauron p130 | RtcB-like Protein | RTCB protein | Acinetobacter baumannii | 8E-146 | IPR001233 | |
| Sauron p131 | NUDIX Hydrolase | DNA mismatch repair protein MutT | Nocardia brasiliensis | 6E-10 | IPR015797, IPR000086, IPR020476, IPR020084 | |
| Sauron p132 | Hypothetical | | | | | |
| Sauron p133 | Hypothetical | | | | | |
| Sauron p134 | Hypothetical | | | | | |
| Sauron p135 | Hypothetical | | | | | |
| Sauron p136 | Hypothetical | | | | | |
| Sauron p137 | Hypothetical | | | | | |
| Sauron p138 | Hypothetical | | | | | |

| Gene | Putative Function | Evidence | | | | |
|---|---|---|---|---|---|---|
| | | Blastp | | | Interpro | TMHMM/Signal P |
| | | Description | Source | E-value | | |
| Sauron p139 | Hypothetical | | | | | |
| Sauron p140 | Hypothetical | | | | | |
| Sauron p141 | Hypothetical | | | | | |
| Sauron p142 | Hypothetical | | | | | |
| Sauron p143 | Hypothetical | | | | | |
| Sauron p144 | Hypothetical | | | | | |
| Sauron p145 | Hypothetical | | | | | |
| Sauron p146 | Hypothetical | | | | | |
| Sauron p147 | Hypothetical | | | | | |
| Sauron p148 | Hypothetical | | | | | |
| Sauron p149 | Hypothetical | | | | | |
| Sauron p150 | Hypothetical | | | | | |
| Sauron p151 | Hypothetical | | | | | |
| Sauron p152 | Hypothetical | | | | | |
| Sauron p153 | Hypothetical | | | | | |
| Sauron p154 | Hypothetical | | | | | |
| Sauron p155 | Hypothetical | | | | | |
| Sauron p156 | Hypothetical | | | | | |
| Sauron p157 | Hypothetical | | | | | |
| Sauron p158 | Hypothetical | | | | | |
| Sauron p159 | Hypothetical | | | | | |
| Sauron p160 | Putative RNA Ligase | putative RNA ligase, DRB0094 family | Aeromonas phage Aes508 | 1E-66 | IPR012646, IPR021122 | |
| Sauron p161 | Hypothetical | | | | | |
| Sauron p162 | Hypothetical | | | | | |
| Sauron p163 | Hypothetical | | | | | |
| Sauron p164 | Hypothetical | | | | | |
| Sauron p165 | Hypothetical | | | | | |
| Sauron p166 | Hypothetical | | | | | |

| Gene | Putative Function | Evidence | | | | |
|---|---|---|---|---|---|---|
| | | Blastp | | | Interpro | TMHMM/Signal P |
| | | Description | Source | E-value | | |
| Sauron p167 | Hypothetical | | | | | |
| Sauron p168 | Type IIA DNA Topoisomerase, GyrA-like | gyrA gene product | Ralstonia phage RSL1 | 0 | IPR002205, IPR013758, IPR013760 | |
| Sauron p169 | Type IIA DNA Topoisomerase, GyrB-like | gyrB gene product | Ralstonia phage RSL1 | 0 | IPR001241, IPR003594, IPR013506, IPR013760, IPR013759, IPR006171, IPR028992, IPR002288, IPR018522, IPR006141 | |
| Sauron p170 | Hypothetical | | | | | |
| Sauron p171 | Hypothetical | | | | | |
| Sauron p172 | Hypothetical | | | | | |
| Sauron p173 | Hypothetical | | | | | |
| Sauron p174 | Hypothetical | | | | | |
| Sauron p175 | Hypothetical | | | | | |
| Sauron p176 | Hypothetical | | | | | |
| Sauron p177 | Hypothetical | | | | | |
| Sauron p178 | Hypothetical | | | | | |
| Sauron p179 | Hypothetical | | | | | |
| Sauron p180 | Hypothetical | | | | | |
| Sauron p181 | Hypothetical | | | | | |
| Sauron p182 | Hypothetical | | | | | |
| Sauron p183 | Hypothetical | | | | | |
| Sauron p184 | Hypothetical | | | | | |
| Sauron p185 | Hypothetical | | | | | |
| Sauron p186 | Hypothetical | | | | | |
| Sauron p187 | Hypothetical | | | | | |
| Sauron p188 | Hypothetical | | | | | |
| Sauron p189 | Hypothetical | | | | | |
| Sauron p190 | Hypothetical | | | | | |
| Sauron p191 | Recombination Endonuclease-like Protein | gp47 recombination endonuclease subunit | Enterobacteria phage T4 | 0.000000005 | IPR029052, IPR024654 | |
| Sauron p192 | Hypothetical | | | | | |
| Sauron p193 | DEAD Type Helicase | | | | IPR011545, IPR027417 | |
| Sauron p194 | Hypothetical | | | | | |

| Gene | Putative Function | Evidence | | | | |
|---|---|---|---|---|---|---|
| | | Blastp | | | Interpro | TMHMM/Signal P |
| | | Description | Source | E-value | | |
| Sauron p195 | Hypothetical | | | | | |
| Sauron p196 | Hypothetical | | | | | |
| Sauron p197 | Hypothetical | | | | | |
| Sauron p198 | Hypothetical | | | | | |
| Sauron p199 | Hypothetical | | | | | |
| Sauron p200 | Hypothetical | | | | | |
| Sauron p201 | Hypothetical | | | | | |
| Sauron p202 | Hypothetical | | | | | |
| Sauron p203 | Hypothetical | | | | | |
| Sauron p204 | Hypothetical | | | | | |
| Sauron p205 | HNH Endonuclease | putative HNH homing endonuclease | Vibrio phage JA-1 | 0.0001 | IPR003615 | |
| Sauron p206 | Hypothetical | | | | | |
| Sauron p207 | Hypothetical | | | | | |
| Sauron p208 | Hypothetical | | | | | |
| Sauron p209 | Hypothetical | | | | | |
| Sauron p210 | Hypothetical | | | | | |
| Sauron p211 | Hypothetical | | | | | |
| Sauron p212 | GroES-like Protein | molecular chaperone GroES | Burkholderia cenocepacia | 2E-21 | IPR020818, IPR011032, IPR018369 | |
| Sauron p213 | Thioredoxin | thioredoxin | Burkholderia sordidicola | 2E-34 | IPR005746, IPR012336, IPR013766, IPR017937 | |
| Sauron p214 | Hypothetical | | | | | |
| Sauron p215 | Hypothetical | | | | | |
| Sauron p216 | Hypothetical | | | | | |
| Sauron p217 | Hypothetical | | | | | |
| Sauron p218 | ATP-Binding Protein | ATP-binding protein | Novosphingobium sp. MBES04 | 1E-95 | IPR027785, IPR027417 | |
| Sauron p219 | Endodeoxyribonuclease | endodeoxyribonuclease | Halosimplex carlsbadense | 9E-10 | IPR012337 | |
| Sauron p220 | Hypothetical | | | | | |
| Sauron p221 | Hypothetical | | | | | |
| Sauron p222 | Hypothetical | | | | | |

| Gene | Putative Function | Evidence | | | | |
|---|---|---|---|---|---|---|
| | | Blastp | | | Interpro | TMHMM/Signal P |
| | | Description | Source | E-value | | |
| Sauron p223 | Metal Dependent Phosphohydrolase-like Protein | putative metal-dependent phosphohydrolase | Pseudomonas phage Lu11 | 3E-12 | IPR006674 | |
| Sauron p224 | HNH Endonuclease | HNH endonuclease | Escherichia phage Av-05 | 2E-27 | IPR003615, IPR010902 | |
| Sauron p225 | DNA Polymerase I | DNA polymerase I | Pseudomonas phage PaBG | 3E-105 | IPR002298, IPR012337, IPR002562, IPR001098 | |
| Sauron p226 | Hypothetical | | | | | |
| Sauron p227 | Hypothetical | | | | | |
| Sauron p228 | DNA Primase | putative DNA primase | Pseudomonas phage Lu11 | 1E-20 | IPR002694, IPR006171 | |
| Sauron p229 | Putative i-spanin | | | | Predicted Signal Peptide | TM:1 7-29 N:in C:out |
| Sauron p230 | Putative o-spanin | | | | Predicted Signal Peptide | SPII:23-24 |
| Sauron p231 | Hypothetical | | | | | |
| Sauron p232 | Hypothetical | | | | | |
| Sauron p233 | Hypothetical | | | | | |
| Sauron p234 | Hypothetical | | | | | |
| Sauron p235 | Hypothetical | | | | | |
| Sauron p236 | Hypothetical | | | | | |
| Sauron p237 | Hypothetical | | | | | |
| Sauron p238 | Thymidylate Synthase | putative thymidylate synthase | Caulobacter phage phiCbK | 1E-46 | IPR003669 | |
| Sauron p239 | Hypothetical | | | | | |
| Sauron p240 | Hypothetical | | | | | |
| Sauron p241 | Hypothetical | | | | | |
| Sauron p242 | Hypothetical | | | | | |
| Sauron p243 | RecA-like Recombinase | protein RecA | Pseudomonas phage PaBG | 1E-85 | IPR013765, IPR027417 | |
| Sauron p244 | Hypothetical | | | | | |
| Sauron p245 | Terminase | putative terminase | Pseudomonas phage PaBG | 3E-92 | | |
| Sauron p246 | RuvC Resolvase-like Protein | putative Holliday junction resolvase | Pseudomonas phage Lu11] | 3E-11 | IPR012337 | |
| Sauron p247 | Hypothetical | | | | | |
| Sauron p248 | Hypothetical | | | | | |
| Sauron p249 | Hypothetical | | | | | |
| Sauron p250 | Hypothetical | | | | | |

| Gene | Putative Function | Evidence | | | | |
|---|---|---|---|---|---|---|
| | | Blastp | | | Interpro | TMHMM/Signal P |
| | | Description | Source | E-value | | |
| Sauron p251 | Hypothetical | | | | | |
| Sauron p252 | Hypothetical | | | | | |
| Sauron p253 | Hypothetical | | | | | |
| Sauron p254 | Homing Endonuclease (GIY-YIG) | | IPR000305, IPR003611 | | | |
| Sauron p255 | Hypothetical | | | | | |
| Sauron p256 | Hypothetical | | | | | |
| Sauron p257 | Hypothetical | | | | | |
| Sauron p258 | Hypothetical | | | | | |
| Sauron p259 | Glucosaminidase | glucosaminidase | Burkholderia glumae | 1E-39 | IPR023346 | |
| Sauron p260 | Hypothetical | | | | | |
| Sauron p261 | Hypothetical | | | | | |
| Sauron p262 | Hypothetical | | | | | |
| Sauron p263 | Hypothetical | | | | | |
| Sauron p264 | Baseplate Wedge Subunit | baseplate wedge subunit | Enterobacteria phage RB69 | 0.000007 | IPR007048, IPR015801 | |
| Sauron p265 | Baseplate Wedge Subunit | putative base plate wedget subunit protein | Pseudomonas phage PaBG | 6E-34 | | |
| Sauron p266 | Hypothetical | | | | | |
| Sauron p267 | Phage Tail Protein | phage tail-collar fiber family protein | Peptoclostridium difficile | 0.0006 | IPR022225 | |
| Sauron p268 | Hypothetical | | | | | |
| Sauron p269 | Hypothetical | | | | | |
| Sauron p270 | Hypothetical | | | | | |
| Sauron p271 | Hypothetical | | | | | |
| Sauron p272 | Hypothetical | | | | | |
| Sauron p273 | Hypothetical | | | | | |
| Sauron p274 | Hypothetical | | | | | |
| Sauron p275 | Hypothetical | | | | | |
| Sauron p276 | Hypothetical | | | | | |
| Sauron p277 | Hypothetical | | | | | |
| Sauron p278 | Hypothetical | | | | | |

| Gene | Putative Function | Evidence | | | | |
|---|---|---|---|---|---|---|
| | | Blastp | | | Interpro | TMHMM/Signal P |
| | | Description | Source | E-value | | |
| Sauron p279 | Hypothetical | | | | | |
| Sauron p280 | Hypothetical | | | | | |
| Sauron p281 | Putative Long Tail Fiber Protein | long tail fiber distal subunit | Enterobacteria phage vB_EcoM_VR5 | 0.00002 | | |
| Sauron p282 | Hypothetical | | | | | |
| Sauron p283 | Putative Endolysin (GH19) | glycoside hydrolase family 19 | Citrobacter freundii | 1E-38 | IPR023346, IPR000726 | |
| Sauron p284 | Putative Antiholin | | | | | TM:1 22-44 N:out C:in |
| Sauron p285 | Putative Type 1 Holin | phage holin | Psychrobacter phage Psymv2 | 1E-12 | | TM:3 10-29, 41-60, 70-92 N:out C:in |
| Sauron p286 | Hypothetical | | | | | |
| Sauron p287 | 5'-3' Exonuclease | | | | IPR029060, IPR002421, IPR020046, IPR020045 | |
| Sauron p288 | Phage Tail Protein | | | | IPR022225 | |
| Sauron p289 | Hypothetical | | | | | |
| Sauron p290 | Hypothetical | | | | | |
| Sauron p291 | NrdA-like Protein | T4 NrdA.1-like protein | Burkholderia phage BcepNazgul | 2E-12 | | |
| Sauron p292 | Hypothetical | | | | | |
| Sauron p293 | Hypothetical | | | | | |
| Sauron p294 | Hypothetical | | | | | |
| Sauron p295 | Hypothetical | | | | | |
| Sauron p296 | DNA Polymerase III-like Protein | DNA polymerase III subunit gamma/tau | actinobacterium SCGC AAA015-D07] | 5E-29 | IPR027417, IPR003593 | |
| Sauron p297 | ATPase Domain Containing Protein | putative ATPase | Pseudomonas phage PaBG | 8E-41 | IPR027417 | |
| Sauron p298 | Hypothetical | | | | | |
| Sauron p299 | Hypothetical | | | | | |
| Sauron p300 | Hypothetical | | | | | |
| Sauron p301 | Hypothetical | | | | | |
| Sauron p302 | DNA Polymerase III Beta Subunit-like | beta clamp domain-like protein | Ralstonia phage RSL1 | 3.46559E-82 | | |
| Sauron p303 | Hypothetical | | | | | |
| Sauron p304 | Hypothetical | | | | | |
| Sauron p305 | Hypothetical | | | | | |
| Sauron p306 | Hypothetical | | | | | |

| Gene | Putative Function | Evidence | | | | |
|---|---|---|---|---|---|---|
| | | Blastp | | | Interpro | TMHMM/Signal P |
| | | Description | Source | E-value | | |
| Sauron p307 | Hypothetical | | | | | |
| Sauron p308 | Hypothetical | | | | | |
| Sauron p309 | ATP-Dependent Helicase | putative DNA/RNA helicase | Pseudomonas phage PaBG | 1E-65 | IPR027417, IPR014001, IPR006935, IPR001650 | |
| Sauron p310 | Hypothetical | | | | | |
| Sauron p311 | Hypothetical | | | | | |
| Sauron p312 | Hypothetical | | | | | |
| Sauron p313 | Hypothetical | | | | | |
| Sauron p314 | Hypothetical | | | | | |
| Sauron p315 | Hypothetical | | | | | |
| Sauron p316 | Hypothetical | | | | | |
| Sauron p317 | Hypothetical | | | | | |
| Sauron p318 | Replicative DNA Helicase | replicative DNA helicase | Pseudomonas phage PaBG | 4E-40 | IPR027417, IPR007694 | |
| Sauron p319 | Hypothetical | | | | | |
| Sauron p320 | Hypothetical | | | | | |
| Sauron p321 | Hypothetical | | | | | |
| Sauron p322 | Hypothetical | | | | | |
| Sauron p323 | Hypothetical | | | | | |
| Sauron p324 | Hypothetical | | | | | |
| Sauron p325 | Hypothetical | | | | | |
| Sauron p326 | Hypothetical | | | | | |
| Sauron p327 | Hypothetical | | | | | |
| Sauron p328 | Hypothetical | | | | | |
| Sauron p329 | Hypothetical | | | | | |
| Sauron p330 | Hypothetical | | | | | |
| Sauron p331 | Hypothetical | | | | | |
| Sauron p332 | Hypothetical | | | | | |
| Sauron p333 | Hypothetical | | | | | |
| Sauron p334 | tRNA His Guanylyltransferase Thg1 | putative tRNA-His guanylyltransferase protein | Caulobacter phage CcrColossus | 1E-48 | IPR007537, IPR024956, IPR025845 | |

| Gene | Putative Function | Evidence | | | | |
|---|---|---|---|---|---|---|
| | | Blastp | | | Interpro | TMHMM/Signal P |
| | | Description | Source | E-value | | |
| Sauron p335 | Hypothetical | | | | | |
| Sauron p336 | Hypothetical | | | | | |
| Sauron p337 | Hypothetical | | | | | |
| Sauron p338 | Hypothetical | | | | | |
| Sauron p339 | Hypothetical | | | | | |
| Sauron p340 | Hypothetical | | | | | |
| Sauron p341 | Hypothetical | | | | | |
| Sauron p342 | Hypothetical | | | | | |
| Sauron p343 | Hypothetical | | | | | |
| Sauron p344 | Hypothetical | | | | | |
| Sauron p345 | Hypothetical | | | | | |
| Sauron p346 | Hypothetical | | | | | |
| Sauron p347 | Hypothetical | | | | | |
| Sauron p348 | Hypothetical | | | | | |
| Sauron p349 | Hypothetical | | | | | |
| Sauron p350 | Hypothetical | | | | | |
| Sauron p351 | Hypothetical | | | | | |
| Sauron p352 | Hypothetical | | | | | |
| Sauron p353 | Hypothetical | | | | | |
| Sauron p354 | Hypothetical | | | | | |
| Sauron p355 | Hypothetical | | | | | |
| Sauron p356 | Hypothetical | | | | | |
| Sauron p357 | Hypothetical | | | | | |
| Sauron p358 | Hypothetical | | | | | |
| Sauron p359 | Hypothetical | | | | | |
| Sauron p360 | Hypothetical | | | | | |
| Sauron p361 | Hypothetical | | | | | |
| Sauron p362 | Hypothetical | | | | | |

| Gene | Putative Function | Evidence | | | | |
|---|---|---|---|---|---|---|
| | | Blastp | | | Interpro | TMHMM/Signal P |
| | | Description | Source | E-value | | |
| Sauron p363 | Hypothetical | | | | | |
| Sauron p364 | Hypothetical | | | | | |
| Sauron p365 | Hypothetical | | | | | |
| Sauron p366 | Hypothetical | | | | | |
| Sauron p367 | Hypothetical | | | | | |
| Sauron p368 | Hypothetical | | | | | |
| Sauron p369 | Hypothetical | | | | | |
| Sauron p370 | Hypothetical | | | | | |
| Sauron p371 | Hypothetical | | | | | |
| Sauron p372 | Hypothetical | | | | | |
| Sauron p373 | T4 RnlA-like RNA ligase and Tail Fiber Attachment Catalyst | RNA ligase | Caulobacter phage Cr30 | 2E-24 | IPR019039 | |
| Sauron p374 | Hypothetical | | | | | |
| Sauron p375 | Hypothetical | | | | | |
| Sauron p376 | Hypothetical | | | | | |
| Sauron p377 | Putative Nucleotidyltransferase | nucleotidyltransferase | Pseudomonas entomophila | 6E-60 | IPR018775 | |
| Sauron p378 | Hypothetical | | | | | |
| Sauron p379 | Hypothetical | | | | | |
| Sauron p380 | Hypothetical | | | | | |
| Sauron p381 | Hypothetical | | | | | |
| Sauron p382 | Hypothetical | | | | | |
| Sauron p383 | Hypothetical | | | | | |
| Sauron p384 | Hypothetical | | | | | |
| Sauron p385 | Hypothetical | | | | | |
| Sauron p386 | Hypothetical | | | | | |
| Sauron p387 | Hypothetical | | | | | |
| Sauron p388 | Hypothetical | | | | | |
| Sauron p389 | Hypothetical | | | | | |
| Sauron p390 | Hypothetical | | | | | |

| Gene | Putative Function | Evidence | | | | |
|---|---|---|---|---|---|---|
| | | Blastp | | | Interpro | TMHMM/Signal P |
| | | Description | Source | E-value | | |
| Sauron p391 | Hypothetical | | | | | |
| Sauron p392 | Hypothetical | | | | | |
| Sauron p393 | Hypothetical | | | | | |
| Sauron p394 | Hypothetical | | | | | |
| Sauron p395 | Hypothetical | | | | | |
| Sauron p396 | Hypothetical | | | | | |
| Sauron p397 | Hypothetical | | | | | |
| Sauron p398 | Hypothetical | | | | | |
| Sauron p399 | Hypothetical | | | | | |
| Sauron p400 | Hypothetical | | | | | |
| Sauron p401 | Hypothetical | | | | | |
| Sauron p402 | Hypothetical | | | | | |
| Sauron p403 | Hypothetical | | | | | |
| Sauron p404 | Hypothetical | | | | | |
| Sauron p405 | Hypothetical | | | | | |
| Sauron p406 | Hypothetical | | | | | |
| Sauron p407 | Hypothetical | | | | | |
| Sauron p408 | Hypothetical | | | | | |
| Sauron p409 | Hypothetical | | | | | |
| Sauron p410 | Hypothetical | | | | | |
| Sauron p411 | Hypothetical | | | | | |
| Sauron p412 | Hypothetical | | | | | |
| Sauron p413 | Bacteriophage-Associated Superinfection Exclusion Protein | putative immunity protein | Burkholderia thailandensis | 0.0002 | IPR016410 | TM:2 15-34, 41-63 N:out C:out |
| Sauron p414 | Bacteriophage-Associated Superinfection Exclusion Protein | putative membrane immunity protein | Escherichia phage vB_EcoP_PhAPEC5 | 0.000002 | IPR016410; predicted signal peptide | TM:2 2-24, 34-56 N:in C:in |
| Sauron p415 | Hypothetical | | | | | |
| Sauron p416 | Hypothetical | | | | | |
| Sauron p417 | Hypothetical | | | | | |
| Sauron p418 | Hypothetical | | | | | |

| Gene | Putative Function | Evidence | | | | |
|---|---|---|---|---|---|---|
| | | Blastp | | | Interpro | TMHMM/Signal P |
| | | Description | Source | E-value | | |
| Sauron p419 | Hypothetical | | | | | |
| Sauron p420 | Hypothetical | | | | | |
| Sauron p421 | Hypothetical | | | | | |
| Sauron p422 | Hypothetical | | | | | |
| Sauron p423 | Hypothetical | | | | | |
| Sauron p424 | Hypothetical | | | | | |
| Sauron p425 | Hypothetical | | | | | |
| Sauron p426 | Hypothetical | | | | | |
| Sauron p427 | Hypothetical | | | | | |
| Sauron p428 | Hypothetical | | | | | |
| Sauron p429 | Hypothetical | | | | | |
| Sauron p430 | Hypothetical | | | | | |
| Sauron p431 | Hypothetical | | | | | |
| Sauron p432 | Hypothetical | | | | | |
| Sauron p433 | Hypothetical | | | | | |
| Sauron p434 | Hypothetical | | | | | |
| Sauron p435 | Hypothetical | | | | | |
| Sauron p436 | Hypothetical | | | | | |
| Sauron p437 | Hypothetical | | | | | |
| Sauron p438 | (p)ppGpp Synthetase | guanosine-3' 5'-bis(diphosphate) 3'-pyrophosphohydrolase | Clostridium sp. CAG:433 | 2E-26 | IPR003607 | |
| Sauron p439 | Hypothetical | | | | | |
| Sauron p440 | Hypothetical | | | | | |
| Sauron p441 | Hypothetical | | | | | |
| Sauron p442 | Hypothetical | | | | | |
| Sauron p443 | Hypothetical | | | | | |
| Sauron p444 | Hypothetical | | | | | |
| Sauron p445 | Hypothetical | | | | | |

| Gene | Putative Function | Evidence | | | | |
|---|---|---|---|---|---|---|
| | | Blastp | | | Interpro | TMHMM/Signal P |
| | | Description | Source | E-value | | |
| Sauron p446 | Hypothetical | | | | | |